Analysis of the genome architecture of the hyperthermophilic archaeon *Thermococcus kodakarensis*

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要旨

ゲノム DNA は細胞内で高度に折りたたまれ、この染色体高次構造は転写・複製・染色体分配といった機構と密接に結びついている。染色体の主要な構成タンパク質は真核生物ではヒストン、バクテリアでは HU と全く異なるが、一様な基本構造を基にゲノム DNA が階層的に折りたたまれている点で両者の染色体構造は共通している。アーキアは真核生物・バクテリアと並ぶ生命の第三のドメインであり、遺伝情報の発現（複製・転写・翻訳）の機構は真核生物に、代謝経路はバクテリアに近い。アーキアには染色体を構成するタンパク質として真核生物のヒストンに相同なもの、バクテリアの HU に相同なもの、アーキア特有の Alba と呼ばれるタンパク質などが存在し、種によってゲノムがコードするタンパク質の組合せが異なる。様々なアーキアのゲノムがどのような高次構造を形成しているかを明らかにすることで、三つのドメインにわたるゲノム構造の共通性あるいは多様性を明らかにできる。本研究ではその第一歩としてヒストンを持つ超好熱性アーキア *Thermococcus kodakarensis* の染色体構造を解析した。

T. kodakarensis の染色体に含まれるタンパク質を質量分析により同定した結果、ヒストン、Alba、TK0471（TrmBL2）、RNA ポリメラーゼ等の DNA 結合タンパク質が含まれることが分かった。TK0471 は転写因子 TrmB と相同な機能未知の DNA 結合タンパク質であった。次に、染色体をミクロコッカルヌクレアーゼで部分消化した後、5%-20%のショ糖密度勾配遠心により構成タンパク質の異なる染色体断片が分離された。原子間力顕微鏡による解析から、ヒストンは DNA 上に beads-on-a-string 構造を、TK0471 は線維状の構造を形成することが示された。また大腸菌で発現させた組換えタンパク質（ヒストンおよび TK0471）を用いて同様の構造が DNA 上に再構成された。ショ糖密度勾配で分離されたそれぞれの染色体断片に含まれる DNA 配列を超並列シークエンサーで同定した結果、ヒストンおよび TK0471 はゲノム上のプロモーター領域にもコーディング領域にも偏りなく存在するが、両者の存在する領域は重複しない傾向があった。以上の結果から、*T. kodakarensis* の染色体上には、構成タンパク質および構造の異なる領域が存在することが明らかとなった。相同組換えにより TK0471 遺伝子を破壊すると染色体の DNA 消化酵素に対する感受性が高まった。また、約 100 個の遺伝子の転写産物量が増加した。TK0471 破壊株における各遺伝子の転写量の上昇と TK0471 タンパク質のプロモーター上の局在とには有意な相関があった。このことから、TK0471 は染色体に多量に存在してゲノム構造を維持すると同時に、プロモーターに結合した場合には転写抑制因子として働くと考えられる。TK0471（TrmBL2）は一部のアーキアとバクテリアの種で保存された新しいタイプの染色体構成タンパク質である。他の種での機能解析によりその機能がより詳細に明らかになることが期待される。

Abstract

Genomic DNA is highly organized and compacted inside the cell. The higher-order chromosome architecture is coupled to cellular processes such as DNA replication, transcription, and chromosome segregation. Although the fundamental architectural protein of the chromosome is different for eukaryotes and bacteria (i.e., histone in eukaryotes and HU in bacteria), eukaryotic chromosomes and bacterial nucleoids both exhibit hierarchical architecture.

Archaea is the third domain of life, distinct from eukaryotes or bacteria. The information processing machineries (DNA replication, transcription, and translation) of archaea are more similar to those of eukaryotes and the metabolic pathways are more similar to those of bacteria. Interestingly, archaeal species encode diverse chromosome architectural proteins such as eukaryotic histone, bacterial HU, as well as archaea-specific Alba. Each archaeal species encodes different combinations of these proteins. Clarification of the chromosome architecture in archaea will lead to the understanding of the general chromosome folding principle in all three domains. As a first step toward this goal, the chromosome architecture of the hyperthermophilic archaeon *Thermococcus kodakarensis* was analyzed in this study.

Histone, Alba, TK0471, and RNA polymerase subunits were identified through mass spectrometry as the major DNA-binding proteins of the *T. kodakarensis* chromosome. TK0471 is a protein previously named TrmB-like 2 (TrmBL2) based on its homology to transcription factors TrmB or Tgr/TrmB-like 1 (TrmBL1), but its specific role has been difficult to identify. Sucrose density gradient sedimentation of a partially digested *T. kodakarensis* chromosome resulted in the separation of chromosome fragments with different protein compositions. Atomic force microscopy revealed that histone forms a “beads-on-a-string” structure, while TK0471 forms a thick fibrous structure on the DNA. High-throughput sequencing of the DNA concentrated with histone or TK0471 showed that these proteins localize to both coding and intergenic regions, but that these areas of localization tend not to overlap. Deletion of the TK0471 gene by homologous recombination results in an alteration of the chromosome into a more nuclease-sensitive state and an increase in the transcript level of approximately 100 genes. The elevation of the transcript level has a significant correlation with the localization of TK0471 to the promoter region of the gene. These results suggest that TK0471 (TrmBL2) is an abundant chromosomal protein that plays dual roles in chromosome architecture and transcriptional regulation. Further analysis in other species may lead to greater understanding of this protein’s function.

Acknowledgements

First and foremost I offer my sincerest gratitude to my supervisor, Dr. Kunio Takeyasu, who has supported me throughout my study with his patience and knowledge whilst allowing me the room to work in my own way. This thesis would not have been completed without his support. He has always emphasized the importance of keeping the big picture in mind, and to study something fundamentally novel. These are important attitudes that I will remember throughout my life. I also appreciate the opportunities he provided me with, like to study abroad as an exchange student, and to attend international conferences. These experiences have broadened my vision towards science.

Next, I would like to express my gratitude to Dr. Shige H. Yoshimura, who was my first direct supervisor when I started my research in the laboratory as an undergraduate student and has been a great advisor since then. I remember the first experiment I conducted with him was to amplify DNA using PCR. He has given me a lot of helpful suggestions, especially when I was writing the manuscript for my research publication. Working with him, I learned the importance of having solid logic in my study.

I sincerely thank all of the current and former members of Takeyasu laboratory for their help and friendship over the years I spent there. The study described in this thesis is based on Dr. Ryosuke L. Ohniwa's study and could not have reached this point without him. He has encouraged me throughout my research with his positive attitude toward science. Drs. Chieko Wada, Kohji Hizeme and Masatoshi Yokokawa encouraged me to publish my research, even when it was not going well and seemed as if it would never end. They have been a pillar of support that has encouraged me to complete my study. I learned a lot about computational analysis and programming from Mr. Toshiyuki Oda. Dr. Minsang Shin has given me many insightful discussions about prokaryotic gene regulation. I thank Ms. Abeer Hasan for English proofreading of my manuscript.

I would like to thank Drs. Rie Matsumi, Haruyuki Atomi, Tadayuki Imanaka and the members in their laboratory for insightful suggestions and discussions about the study of the archaeal species. This collaborative study would not have been possible without them. I also thank Dr. Katsuhiko Shirahige and Dr. Takehiko Itoh for their support and helpeful suggestions about DNA sequencing, which constitutes an important part of this thesis.

Next, I would also like to thank the people I worked with at the Salk Institute for Biological Studies in La Jolla, USA. Professor Takeyasu provided me with the opportunity to study there as an exchange student. There I worked mainly with the

postdoctoral researcher Dr. Marcela Raices under the supervision of Dr. Andrew Dillin and Dr. Jan Karlseder. I learned to be aware of the biological and/or medical relevance of my own study, and to always think about how I can contribute to move the research field forward.

I would like to thank the Graduate School of Biostudies and the “Life Science English Communication Program” for their support to send me to the Gordon Research Conference on Archaea in 2009. I would also like to thank the Ministry of Education, Culture, Sports, Science and Technology of Japan and the “Academic Frontiers Student Exchange Promotion Program” for their support for me to study abroad as an exchange student.

Last but not least, I thank my parents, who have educated, supported and encouraged me to pursue my interests. Without their continuous support, it was not possible to complete my work. I also thank all my friends. Without the time I spent with them outside the laboratory, I could not have maintained a healthy mind to concentrate on science.

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2011

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(1) Peer-Reviewed Research Articles

1. K. Hizume, S.H. Yoshimura, H. Maruyama, J. Kim, H. Wada & K. Takeyasu (2002) Chromatin Reconstitution: Development of a Salt-dialysis Method Monitored by

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4. H. Maruyama, M. Shin, T. Oda, R Matsumi, R.L. Ohniwa, T. Itoh, K. Shirahige, T. Imanaka, H. Atomi, S.H. Yoshimura, K. Takeyasu (2011). Histone and TK0471/TrmBL2 form a novel heterogeneous genome architecture in the hyperthermophilic archaeon *Thermococcus kodakarensis*. ***Mol Biol Cell***.22(3): 386-398

(2) Book chapter

1. K. Takeyasu, H. Maruyama, Y. Suzuki, K. Hizume and S.H. Yoshimura (2010) Modern Atomic Force Microscopy and its application to the study of genome architecture. ***Scanning probe microscopy in nanoscience and nanotechnology***. Springer pp. 723 - 756

Presentations at Scientific Conferences

(1) International conferences

1. H. Maruyama, S.H. Yoshimura, R. Ohki, F. Ishikawa & K. Takeyasu （2002/10 Nigata, Japan） Working model of telomeric repeat binding factor 2 in t-loop formation. International symposium on chromosome research at the nano-era
2. S.H. Yoshimura, K. Hizume, H. Maruyama, J. Kim, H. Wada & K. Takeyasu (2002/11 Pusan, Korea) Nano-biology of the Gene: Structural analysis of reconstituted chromatin by Atomic Force Microscopy. ***International Symposium on Nanobioscience***
3. S.H. Yoshimura, H. Maruyama, R. Ohki, F. Ishikawa & K. Takeyasu (2002/12 San Francisco) Working model of telomeric repeat binding factor 2 in t-loop formation. 42nd annual meeting of the American Society for Cell Biology
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5. M. Raices, H. Maruyama, R. Verdun, C. Haggblom, S. Compton, J Griffith, A. Dillin, J. Karlseder (2006 Madrid, Spain) Telomere structure and function in C. elegans. ***CNIO Cancer conference: Telomeres & Telomerase***
6. H. Maruyama, R.L. Ohniwa, R. Matsumi, H. Atomi, T. Imanaka, K. Takeyasu.

(2008/5 Kyoto, Japan) Analysis of chromatin structure of Thermococcus kodakaraensis KOD1 strain. ***The 3rd NTU-Kyoto U student mini-Symposium on molecular and cell biology*** （Poster award）

7. A. Shiraishi, M. Kumeta, H. Maruyama, R.L. Ohniwa, H. Takahashi, K. Hizume and K. Takeyasu (2008/6, Seattle) Atomic Force Microscopy Reveals a Step-wise Genome Folding in Prokaryote. ***International Scanning Probe Microscopy Conference 2008***
8. H. Maruyama, S. Iwano, R. Matsumi, R.L. Ohniwa, T. Imanaka, H. Atomi and K. Takeyasu (2009/7 Waterville Valley, USA) The genome of a hyperthermophilic archaeaon Thermococcus kodakaraensis consists of distinct structural domains enriched with histone or TK0471. ***Gordon Research Conference, Archaea: Ecology, Metabolism & Molecular Biology*** (Received "Second place poster award")

(2) Domestic meetings

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3. H. Maruyama, R.L. Ohniwa, R. Matsumi, H. Atomi, T. Imanaka, K. Takeyasu (2008/12 Kobe, Japan) Analysis of the chromatin structure of the hyperthermophilic Archaeaon Thermococcus kodakaraensis. ***Biochemistry and Molecular Biology Society of Japan meeting 2008*** (Oral presentation)
4. H. Maruyama, R.L. Ohniwa, R. Matsumi, S. Iwano, H. Atomi, T. Imanaka, K. Takeyasu (2009/3 Tokyo, Japan) Analysis of higher-order chromosome structure and the role of a DNA-binding protein TK0471 in the hyperthermophilic Archaeaon Thermococcus kodakaraensis. ***The 3rd annual meeting of the Society of Genome Microbiology, Japan*** (Oral presentation)
5. H. Maruyama, M. Shin, S. Iwano, R. Matsumi, R.L. Ohniwa, T. Itoh, K. Shirahige, T. Imanaka, H. Atomi, K. Takeyasu (2009/10 Tokyo, Japan) Analysis of the chromosome structure of a hyperthermophilic archaeon Thermococcus kodakaraensis. ***10th Japanese Society for Extremophiles annual meeting***
6. H. Maruyama, M. Shin, H. Atomi, R.L. Ohniwa, S.H. Yoshimura, K. Takeyasu (2009/12 Yokohama, Japan) Higher-order structure of archaeal chromosome ***The***

32nd annual meeting of the Molecular Biology Society of Japan (Oral presentation at the workshop "New frontier of functional regulation in the nucleoid with high-ordering structure")

7. H. Maruyama, M. Shin, R.L. Ohniwa, T. Itoh, K. Shirahige, T. Imanaka, H. Atomi and K. Takeyasu (2010/3 Fukuoka, Japan) Chromosome of the hyperthermophilic archaeon Thermococcus kodakaraensis is organized into heterogeneous structure. ***The 4th annual meeting of the Society of Genome Microbiology, Japan***

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1. Introduction

1-1 Eukaryotic chromosome architecture

It is necessary for all kinds of cells to organize the chromosome structure in order to achieve the compaction of genomic DNA inside the cell. In eukaryotic cells, genomic DNA is constrained into nucleosomes, in which 146 bp of DNA is wrapped around a core histone octamer (Luger *et al.*, 1997). The array of nucleosomes, which is called "beads-on-a-string", is further organized into higher-order structures (Figure 1A) with the aid of other proteins and/or environmental factors such as ionic strength (Kobori *et al.*, 2007). Higher-order chromosome structure and dynamics play important roles in the regulation of processes such as transcription, replication and chromosome condensation (Ehrenhofer-Murray, 2004).

The eukaryotic histone octamer consists of two of each core histone; H2A, H2B, H3 and H4. All core histones carry lysine-rich amino-terminal tail regions that extend outside the nucleosome core (Luger *et al.*, 1997) and undergo post-transcriptional modifications including methylation, acetylation, and phosphorylation (Kouzarides, 2007). The histone tail modification leads to alteration in the chromatin structure by affecting electrostatic interactions between the histones and DNA, and/or through creating binding epitopes with which to recruit other proteins (Taverna *et al.*, 2007; Arya and Schlick, 2009). Linker histones (H1, H5 and other subtypes) are also believed to contribute to the formation of higher-order chromosome structures (30-nm fiber) by binding to the nucleosome dyad, the entry-exit region formed by linker DNA (Bednar *et al.*, 1998).

The most dramatic change of chromosome structure occurs during mitosis, in which chromosomes undergo a high degree of condensation. Condensin complex plays an important role in this process (Hirano, 2006; Wood *et al.*, 2010). The condensin complex consists of structural maintenance of chromosomes (SMC) subunits and non-SMC subunits. Common structural characteristics of SMC proteins are the DNA-binding domains and the ATP-binding domains connected with a long coiled-coil and a flexible center hinge (Hirano, 2006). Other SMC protein-containing complexes, such as cohesin and SMC5-SMC6, also play important roles in chromosome dynamics. The cohesin complex plays a role in sister chromatid cohesion and regulation of gene expression (Wendt *et al.*, 2008; Nasmyth and Haering, 2009; Wendt and Peters, 2009), while the SMC5-SMC6 complex is implicated in DNA repair (De Piccoli *et al.*, 2006; De Piccoli *et al.*, 2009).

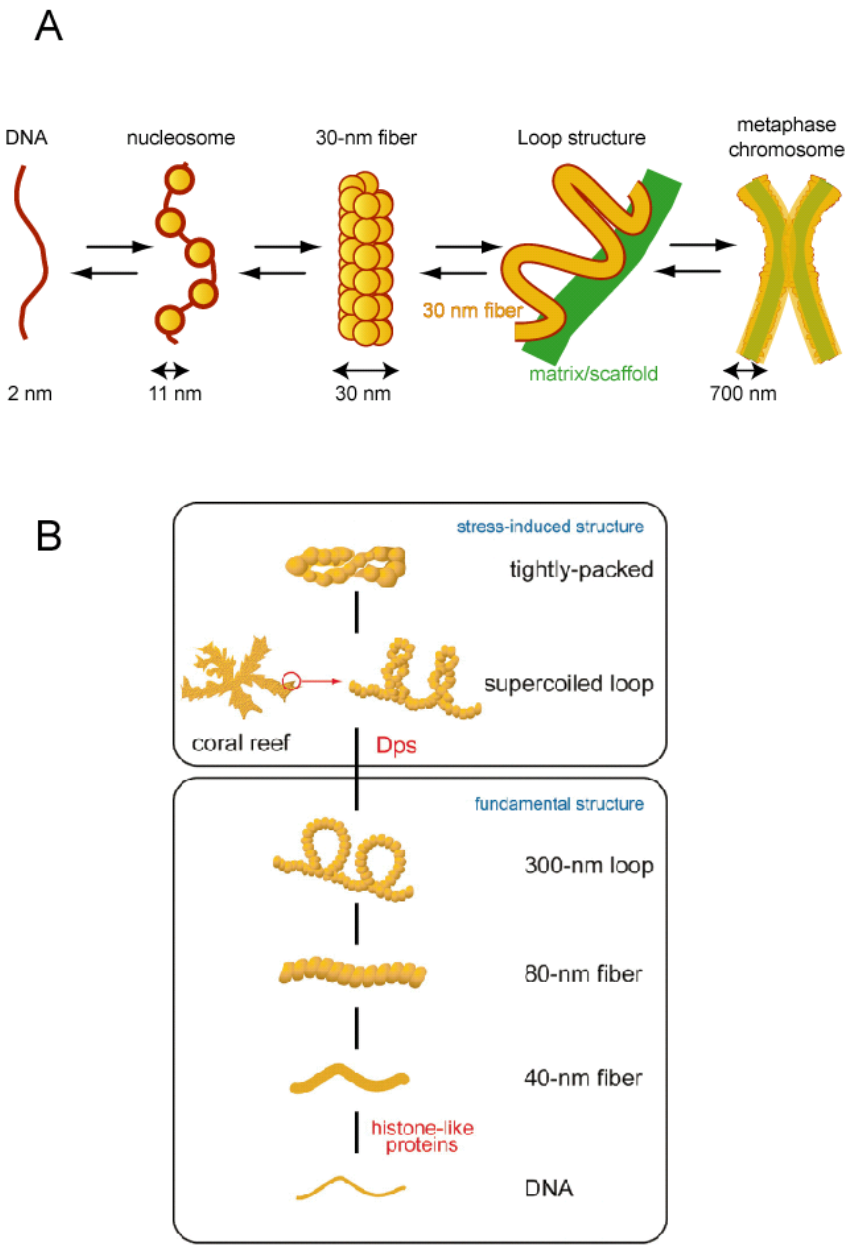

Figure 1

Figure 1. Eukaryotic and bacterial chromosome architecture

Hierarchical architecture of (A) eukaryotic chromosome (Hizume, 2005) and (B) bacterial nucleoid (Kim *et al.*, 2004).

1-2 Bacterial nucleoid

Prokaryotes consist of two domains, Bacteria and Archaea. Cells in these two domains look similar in morphology, but are fundamentally different from each other in the following aspects. First, archaea have membranes composed of glycerol-ether lipids, whereas bacteria (and eukaryotes) have membranes composed mainly of glycerol-ester lipids (De Rosa *et al.*, 1986). Second, whereas peptidoglycan is a standard component of all bacterial cell walls, all archaeal cell walls lack peptidoglycan and instead are composed of pseudopeptidoglycan, polysaccharides, glycoprotein, or surface-layer (S-layer) proteins, depending on species (Kandler and Konig, 1998). Third, organization of chromosome structure has important differences between the two domains (see below).

Bacterial genomes are packed into a region referred to as a 'nucleoid' (Robinow and Kellenberger, 1994). Studies on proteins involved in the genome architecture have revealed that bacteria lack histones (Zimmerman, 2006). *Escherichia coli* is one of the best-studied bacteria, and a significant effort has been made to understand its nucleoid structure. *E. coli* has a set of DNA-binding proteins including RNA polymerases and about 300 types of transcription factors (Zimmerman, 2006). The amount of each nucleoid protein in a cell changes depending on growth conditions and influences the genome structure (Ali Azam *et al.*, 1999; Kim *et al.*, 2004). Among them, HU (heat-unstable nucleoid protein) is one of the most abundant proteins in *E. coli* (Ali Azam *et al.*, 1999); IHF (integration host factor), H-NS (histone-like nucleoid structural protein), Fis (factor for inversion stimulation), Hfq (host factor for phage RNA Qb replication), StpA (suppressor of T4 td mutant phenotype A) and Dps (DNA-binding protein from starved cells) are the major small nucleoid proteins (Azam and Ishihama, 1999). HU and Dps proteins are widely spread throughout the bacterial domain, whereas the other nucleoid proteins are specific to Gamma-proteobacteria including *E. coli* (Takeyasu *et al.*, 2004).

Similar to the eukaryotic chromosome, the bacterial nucleoid also exhibit a hierarchical higher-order architecture and dynamic structural changes (Kim *et al.*, 2004; Ohniwa *et al.*, 2007) (Figure 1B). An example of the structural dynamics is Dps-dependent nucleoid condensation in the stationary phase or under oxidative stress (Kim *et al.*, 2004; Ohniwa *et al.*, 2007). Under these conditions, the amount of Dps in cells dramatically increases, leading to nucleoid compaction (Ali Azam *et al.*, 1999; Ohniwa *et al.*, 2007).

The SMC family proteins are also conserved through the prokaryote boundary. Most prokaryotes possess only a single SMC protein that forms a homodimer. Examples

are MukB in *E. coli* (Niki *et al.*, 1991) and BsSMC in *Bacillus subtilis* (Oguro *et al.*, 1996). These SMC proteins have little sequence similarity to the eukaryotic SMCs, but share common structural characteristics with eukaryotic SMC proteins (Niki *et al.*, 1992). Bacterial SMC proteins have been shown to play roles in chromosome segregation as well as in DNA repair (Graumann and Knust, 2009). Whether prokaryotic SMC also plays a role in chromosome dynamics needs to be determined.

1-3 Archaeal DNA-binding proteins and chromosome architecture

Archaea are distinct from both Bacteria and Eukaryotes, and thus constitute the third domain of life (Figure 2A). This domain is currently divided into two main phyla, Crenarchaeota and Euryarchaeota, along with several other newly proposed phyla such as Korarchaeota and Thaumarchaeota (Woese *et al.*, 1990; Gribaldo and Brochier, 2009). Archaeal species possess a mixture of bacterial and eukaryotic features. For example, the DNA replication, transcription and translation machineries of archaea are more similar to those of eukaryotes, while the genes involved in metabolic processes show more similarities to their bacterial counterparts (Koonin *et al.*, 1997; Smith *et al.*, 1997).

Archaea are interesting organisms to study chromosome organization because of the diversity of chromosomal proteins among species (Table 1 and Figure 2B). Most crenarchaeal species encode a protein called Alba (acetylation lowers binding affinity; also known as Ssh10b, Sso10b and Sac10b, depending on the species). Alba can constitute up to ~4% of the total cellular proteins in *Sulfolobus* (Xue *et al.*, 2000) and is considered a major chromosomal protein. The affinity of Alba to DNA increases upon deacetylation by the silencing protein Sir2 (Bell *et al.*, 2002). It has been proposed that its dynamic association to and dissociation from DNA is involved in transcriptional regulation and modulation of chromatin structure (Bell *et al.*, 2002). However, there is a controversy about the real function of Alba because it binds not only to DNA, but also to RNA (Aravind *et al.*, 2003; Guo *et al.*, 2003). Some euryarchaeal species also encode Alba, although the protein is less abundant in these cells. It is unclear to what extent Alba plays a role in chromosome architecture in euryarchaeal species.

In 1990, a protein homologous to eukaryotic histones was reported in the methanogen, *Methanothermus fervidus* (Sandman *et al.*, 1990). This was the first example of a histone homolog in prokaryotes. Searches in genomic sequences as well as biochemical studies revealed that most euryarchaeal species encode histone proteins. Rare exceptions include the species in the order Thermoplasmatales, which encode the bacterial HU homolog but not histones (Table 1).

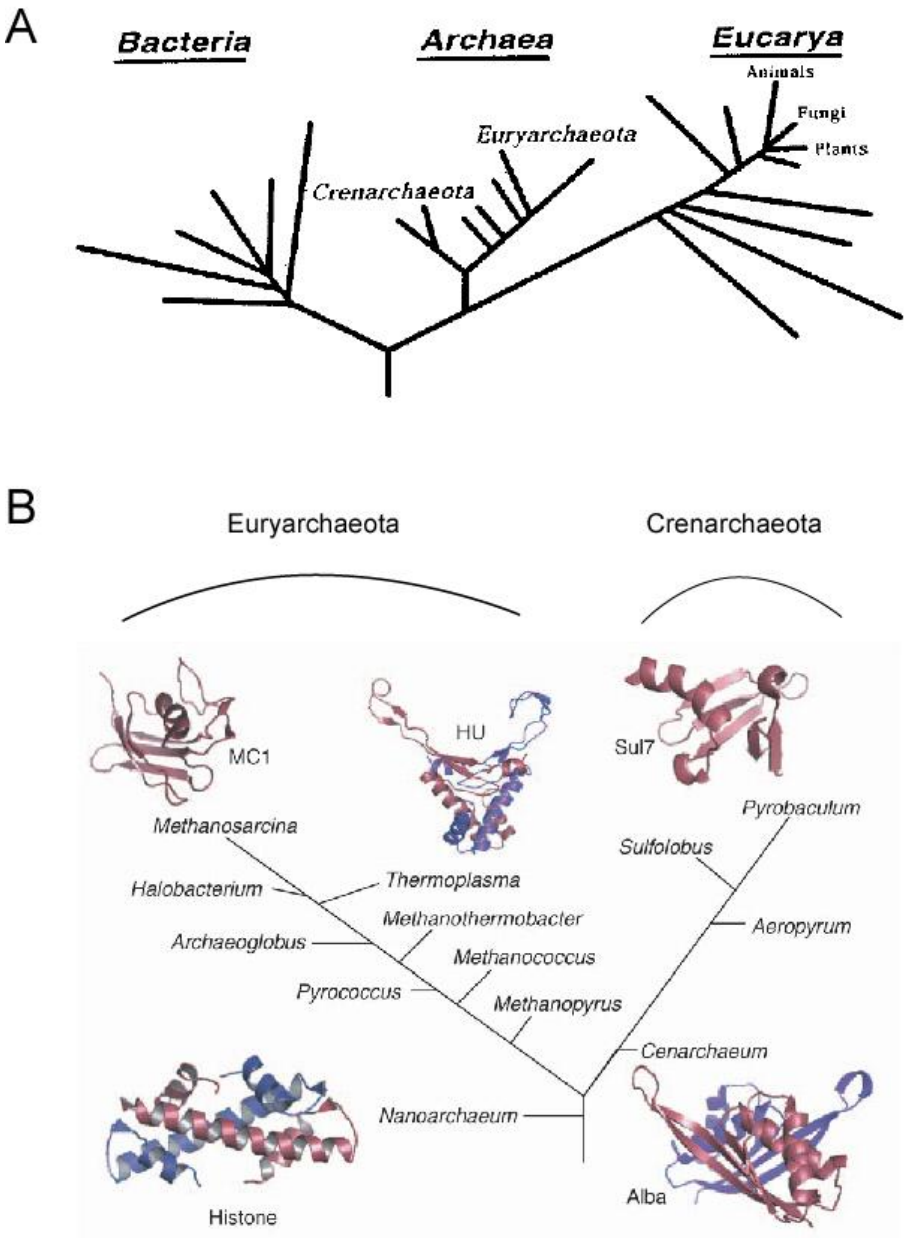

Figure 2

Figure 2. Archaea and chromatin proteins

(A) Phylogenetic tree of the three domains of life, Eukaryotes, Bacteria, and Archaea (Woese, 2000). The two major phyla in archaea Euryarchaeaota and Crenarchaeota are indicated. (B) Distribution of different chromatin proteins among archaeal species (Sandman and Reeve, 2005).

Table 1. Number of proteins homologous to known chromosomal proteins (e value < 0.01 in BLAST search)

Order	Genus	Species	Histone	HU	Alba
Euryarchaeota	Methanocaldococcus	Methanocaldococcus jannaschii	4		1
		Methanocaldococcus vulcanius	3		1
		Methanocaldococcus sp. FS406-22	3		1
		Methanocaldococcus infernus	1		
	Methanococcus	Methanococcus maripaludis S2	2		1
		Methanococcus aeolicus	2		1
		Methanococcus vannielii	2		1
		Methanococcus voltae	2		1
	Methanosarcina	Methanosarcina acetivorans	1		
		Methanosarcina barkeri	1		
		Methanosarcina mazei	1		
	Methanococcoides	Methanococcoides burtonii	1		
	Methanohalophilus	Methanohalophilus mahii	1		
	Methanohalobium	Methanohalobium evestigatum	1		
	Methanosaeta	Methanosaeta thermophila	1		1
	Methanospirillum	Methanospirillum hungatei	5		1
	Methanocorpusculum	Methanocorpusculum labreanum	1		1
	Methanoculleus	Methanoculleus marisnigri	2		1
	Methanoplanus	Methanoplanus petrolearius	1		1
	Methanoregula	Candidatus Methanoregula boonei	1		1
	Methanosphaerula	Candidatus Methanosphaerula palustris	1		1
	Methanocella	Methanocella paludicola	2		1
	Methanobacterium	Methanothermobacter thermautotrophicus	3		1
		Methanothermobacter marburgensis	3		1
	Methanosphaera	Methanosphaera stadtmanae	6		1
	Methanobrevibacter	Methanobrevibacter smithii ATCC 35061	3		1
		Methanobrevibacter ruminantium	6		
	Methanothermus	Methanothermus fervidus	2		1
	Methanopyrus	Methanopyrus kandleri	2		2
	Archaeoglobus	Archaeoglobus fulgidus	2		2
		Archaeoglobus profundus	2		2
	Ferroglobus	Ferroglobus placidus	2		2
	Halobacterium	Halobacterium sp. NRC-1	1		
		Halobacterium salinarum R1	1		
	Haloarcula	Haloarcula marismortui	1		
	Haloquadratum	Haloquadratum walsbyi	1		
	Natronomonas	Natronomonas pharaonis	1		
	Halorubrum	Halorubrum lacusprofundi	1	1	
	Halorhabdus	Halorhabdus utahensis	1		
	Halomicrobium	Halomicrobium mukohataei	1		
	Haloterrigena	Haloterrigena turkmenica	1		
	Natrialba	Natrialba magadii	1		
	Haloferax	Haloferax volcanii	1		
	Halalkalicoccus	Halalkalicoccus jeotgali	1		
	Thermoplasma	Thermoplasma acidophilum		1	1
		Thermoplasma volcanium		1	1
	Picrophilus	Picrophilus torridus		1	1
	Pyrococcus	Pyrococcus horikoshii	2		1
		Pyrococcus abyssi	2		1
		Pyrococcus furiosus	2		1
	Thermococcus	Thermococcus kodakaraensis	2		1
		Thermococcus onnurineus	2		1
		Thermococcus gammatolerans	2		1
		Thermococcus sibiricus	2		1
	Aciduliprofundum	Aciduliprofundum boonei		1	1
	Rice Cluster I	Uncultured methanogenic archaeon RC-I	2		1
Nanoarchaeota	Nanoarchaeum	Nanoarchaeum equitans	2		1

Table 1 continued

Crenarchaeota	Aeropyrum	Aeropyrum pernix				2
	Staphylothermus	Staphylothermus marinus				2
		Staphylothermus hellenicus				2
	Ignicoccus	Ignicoccus hospitalis				2
	Desulfurococcus	Desulfurococcus kamchatkensis				2
	Thermosphaera	Thermosphaera aggregans				2
	Ignisphaera	Ignisphaera aggregans				3
	Hyperthermus	Hyperthermus butylicus				2
	Sulfolobus	Sulfolobus solfataricus				2
		Sulfolobus tokodaii				2
		Sulfolobus acidocaldarius				2
		Sulfolobus islandicus L.S.2.15				2
	Metallosphaera	Metallosphaera sedula				2
	Pyrobaculum	Pyrobaculum aerophilum				1
		Pyrobaculum islandicum				1
		Pyrobaculum calidifontis				1
		Pyrobaculum arsenaticum				1
	Caldivirga	Caldivirga maquilingensis	1			1
	Thermoproteus	Thermoproteus neutrophilus				1
	Vulcanisaeta	Vulcanisaeta distributa	1			1
	Thermofilum	Thermofilum pendens	1			3
	Acidilobus	Acidilobus saccharovorans				2
Thaumarchaeota	Nitrosopumilus	Nitrosopumilus maritimus	1			2
Korarchaeota	Korarchaeum	Candidatus Korarchaeum cryptofilum	2			1

Table 1. Distribution of chromatin proteins in archaeal species

Number of genes encoding proteins homologous to chromatin proteins in each species are listed (e value < 0.01 in BLAST search). Queries for the searches were, *M. fervidus* histone (HMf), *E. coli* HU (hupA), and *S. solfataricus* Alba.

Although the structure of the histone fold motif is quite similar between eukaryotic and archaeal histones, there are several differences between the two. The archaeal histones consist solely of the histone-fold motif (Sandman and Reeve, 2005) and lack the N- and C-terminal tails. Unlike eukaryotic histones, which form octamers, archaeal histones form tetramers (Pereira *et al.*, 1997). It has been shown that approximately 120 bp of DNA can wrap around an archaeal histone tetramer *in vitro* (Tomschik *et al.*, 2001), which is shorter than that in the eukaryotic nucleosome.

Many studies have supported the conclusion that archaeal histones and genomic DNA form nucleosome structures *in vivo* (Shioda *et al.*, 1989; Pereira *et al.*, 1997). However, the lack of histone tails in archaea implies that the higher-order structure and the function of the genome may be regulated in a way different from those in eukaryotes. Other proteins might contribute to the chromosome architecture in these species.

1-4 Aim of this thesis

Chromosome structure and its regulation have been studied in detail in eukaryotes and bacteria. However, the differences in protein components and chromosome architecture between bacterial and eukaryotic chromosomes have made it difficult to understand the general principle of chromosome architecture and dynamics. Archaea are the ideal organisms to fill this gap. An understanding of the organization and dynamics of the archaeal chromosome may provide new insights into the common folding mechanism among all three domains of life.

Among archaea, euryachaeal species are of special interest in relation to the eukaryotic chromosome structure because they use the same building blocks of chromosome as eukaryotes do, i.e. histone. Besides histones, archaeal RNA polymerase and replication machinery are more similar to eukaryotic than bacterial ones (Langer *et al.*, 1995; Decanniere *et al.*, 1996; Hirata *et al.*, 2008b). Therefore, chromatin structures in euryarchaeal species can be viewed as a primitive form of the eukaryotic counterpart, not only in terms of the fundamental structural unit, but also in terms of the whole information processing system, including transcription and replication. A better understanding of the euryarchaeal chromatin architecture could reveal the minimum requirements for the histone-based chromosome system, and will provide insights into what makes eukaryotic chromosome different from those of prokaryotes.

In this thesis, I focused on the histone-encoding euryarchaeon *Thermococcus kodakarensis* as the first step towards the understanding of archaeal chromosome architecture. In addition to the reasons described above, there are several advantages of

using *T. kodakarensis* as a model. 1) *T. kodakarensis* is one of the few archaeal species in which a gene manipulation system has been established (Sato *et al.*, 2003, 2005; Leigh *et al.*, 2011). This is a great advantage when performing genetic analysis. 2) Biochemical properties of histones (Higashibata *et al.*, 1999; Higashibata *et al.*, 2003) as well as the transcription (Santangelo *et al.*, 2007; Hirata *et al.*, 2008a) and replication (Myllykallio *et al.*, 2000; Matsunaga *et al.*, 2001; Matsunaga *et al.*, 2007; Yoshimochi *et al.*, 2008) machineries have been studied and accumulated in *T. kodakarensis* and/or closely related *Pyrococcus* species. Taking advantage of this euryarchaeon, I studied the protein component of the chromosome, examined the structural and functional differences between different chromosomal proteins, and elucidated how the chromosome structure is organized in the cell.

2. Materials and methods

2-1 Strains and growth conditions

Thermococcus kodakarensis KOD1 was cultivated under anaerobic conditions at 85°C in the nutrient-rich medium ASW-YT, supplemented with 0.2% elemental sulfur (ASW-YT-S^0). ASW-YT medium was composed of a 1.25-fold dilution of artificial seawater (Robb and Place, 1995) (0.8x ASW [16 g/l NaCl, 2.4 g/l $MgCl_2$·6H2O, 4.8 g/l $MgSO_4$·$7H_2O$, 0.8 g/l $(NH_4)_2SO_4$, 0.16 g/l $NaHCO_3$, 0.24 g/l $CaCl_2$·$2H_2O$, 0.4 g/l KCl, 0.34 g/l KH_2PO_4, 40 mg/l NaBr, 16 mg/l $SrCl_2$·$6H_2O$, 8 mg/l Fe(NH_4) citrate]), 5.0 g/L of yeast extract and 5.0 g/L of tryptone. Resazurin was added at a concentration of 0.8 mg/L. Prior to inoculation, Na2S was added to the medium until it became transparent. A fresh medium was inoculated with a pre-culture in the stationary phase and cells were harvested at log or stationary phase. Construction of the deletion strain is described in Supplemental Materials.

2-2 On-substrate cell lysis of *T. kodakarensis* cells

KOD1 cells were harvested and centrifuged for 1 min at 10,000 rpm at 4°C. Cells were washed and resuspended in 0.8x ASW. Cell density was adjusted to OD_{660} = ~0.5. Cell suspension (50 µl) was applied to a cover glass (15 mm round, Matsunami Glass Ind., Kishiwada, Japan) and left for 10 min at 25°C. Liquid was blown off with nitrogen or difluoroethane (HFC-152a) gas. Cells on the cover glass were lysed through addition of Milli-Q® water and incubation for 10 min at 25°C. Liquid was blown off with gas and samples were subjected to AFM for observation. For DAPI-staining, lysed cells attached to a cover glass were stained by adding 0.8x ASW containing DAPI onto the cover glasses (18 x 18 mm, Matsunami). Intact cells were stained by adding DAPI to the culture.

2-3 Construction of the *T. kodakarensis* ΔTK0471 strain

Deletion of the TK0471 gene was performed as described previously (Sato *et al.*, 2005). The plasmid DNA used for disruption of the TK0471 genes was constructed as follows. A DNA fragment containing the TK0471-coding region together with its flanking regions (~1000 bp) was amplified from genomic DNA by PCR using the primer set tk403475-for (5'-CAGGAACTCGGCGAAAAGTA-3') and tk406333-rev (5'-GGACGAGGCGAGTCAAGATA-3'), and inserted into the SmaI site of the plasmid pUD3, which contains a *pyrF* marker gene cassette inserted into pUC118 plasmid (Yokooji *et al.*, 2009). Using the plasmid as the template, inverse PCR was

performed with the primer set tk404501-rev (5'-CTTTACCACCACCTAATTTTC-3') and tk405294-for (5'- TGATCCCTTCTCTCTGTTCT–3') to remove the TK0471 coding region. The amplified fragment was self-ligated, resulting in the plasmid for TK0471 disruption (pUD3-dlTK0471). The *T. kodakarensis* uracil-auxotroph strain known as KUW1 (Δ*pyrF*, Δ*trpE*) was used as the host strain. After transformation, a *pyrF* $^{+}$ strain exhibiting uracil prototrophy was selected. Next, *pyrF* pop-out recombinants were positively selected on a rich plate medium supplemented with 0.75% 5-fluoroorotic acid (5-FOA). The genotypes of the TK0471 locus were confirmed through PCR amplification using the primer set tk404227-for (5'-TGCTGTCCCATTCTGTCTTTT–3') and tk406043-rev (5'-GACAGAATAAGGCACTCCCG-3'). Genotypes were also confirmed through Southern blotting analyses. One hundred nanograms of genomic DNA from KUW1 and a transformant were digested with BamHI and EcoRI, separated by 0.8% agarose gel electrophoresis and transferred to a Hybond-N+ nylon membrane (GE Healthcare, Milwaukee, WI, USA). DNA probes for hybridization were labeled with ^{32}P using the Prime-a-Gene Labeling System (Promega, Madison, WI, USA) and the radioactivity was visualized using a FLA-7000 phosphorimager (Fujifilm, Tokyo, Japan). The constructed ΔTK0471 strain (Δ*pyrF*, Δ*trpE*, *ΔTK0471*) was designated as KCP1.

2-4 Atomic force microscopy

Samples were observed under a Nanoscope IIIa or IV (Digital Instruments, Santa Barbara, CA, USA) in tapping mode using OMCL-AC160TS probe (Olympus, Tokyo, Japan). Either type E or type J scanners were used depending on the size of the observed area. Images were analyzed using Nanoscope software. Widths of the chromatin fibers were calculated based on apparent bottom-to-bottom distance of particles, using the equation described previously for the same probe; S = 0.75W - 16.14, where W is the apparent measured bottom-to-bottom distance, and S is the estimated actual width of samples (Ohniwa *et al.*, 2007).

2-5 Preparation of chromatin fraction

Chromatin fraction was obtained by the method described previously (Matsunaga *et al.*, 2001) with a slight modification. *T. kodakarensis* cells were harvested in the log phase or the stationary phase. Samples were washed once with 0.8x ASW. Cell suspensions (~10^{10} cells per milliliter) were disrupted by the addition of extraction buffer (25 mM HEPES (pH 7.0), 15 mM $MgCl_2$, 100 mM NaCl, 0.4 M Sorbitol and 0.5% Triton X-100). After incubating for 10 min at 4°C, soluble proteins (supernatant) and a

chromosomal DNA-enriched insoluble fraction (pellet) were separated by centrifugation at 14,000 g for 20 min. The insoluble chromatin fraction, containing DNA and chromatin-associated protein, was washed with the extraction buffer and frozen at –20°C until further use.

2-6 Micrococcal nuclease digestion of *T. kodakarensis* chromatin

A chromatin fraction equivalent to that derived from ~30 ml of culture was suspended in 600 µl of MNase buffer (20 mM Tris-HCl (pH 7.4), 5 mM NaCl, 2.5 mM $CaCl_2$) and pre-incubated at 37°C. Cell lysate in MNase buffer was separated into portions of 100 µl each. Micrococcal nuclease (Worthington Biochemical, Lakewood, NJ, USA) was added in increasing amounts (0, 0.3, 1, 3, 10, and 30 units) to 100 µl of lysate and incubated for 10 min at 37°C. The reaction was quenched by adding 11 µl of 10x STOP mix (2% SDS, 100 mM EDTA (pH 8.0), 100 mM EGTA). One microliter of Proteinase K (20 mg/ml, Invitrogen, Carlsbad, CA, USA) was added and the mixture was incubated for 3 hours at 37°C. DNA was extracted with Phenol / Chloroform / Isoamyl alcohol (25:24:1, Nacalai Tesque, Kyoto, Japan) and precipitated with ethanol. The pellet was resuspended in TNE buffer (10 mM Tris-HCl (pH 8.0), 100 mM NaCl, 1 mM EDTA). RNase A (Roche Applied Science, Mannheim, Germany) was added to a final concentration of 5 µg/ml and the mixture was incubated for 2 hours at 37°C. Proteinase K (20 mg/ml) was added to a final concentration of 0.1 mg/ml and the mixture was incubated for 1 hour at 37°C. DNA was then extracted as described above and dissolved in TE buffer. For electrophoresis, 1 or 2 µg of DNA was separated on 2.5% agarose gel in 0.5x TBE or in 4% NuSieve® GTG® agarose (Lonza Group Ltd., Basel, Switzerland) gel in 1x TBE. DNA was stained using ethydium bromide or SYBR Gold (Invitrogen) after gel electrophoresis. For simultaneous treatment of chromatin with MNase and RNase A, RNase A was added to a concentration of 10 µg/µl to the MNase reaction described above.

2-7 Mass spectrometry

Proteins in the chromatin fraction were separated through SDS-PAGE on a 5% - 20% gradient polyacrylamide gel (Bio-Rad Laboratories, Hercules, CA, USA) after digestion with micrococcal nuclease (MNase, Worthington Biochemical, Lakewood, NJ, USA). Protein bands were excised from the gel and digested in-gel with trypsin. The matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) mass spectra measurements were performed on an AXIMA-CFR spectrometer (Shimadzu Biotech, Kyoto, Japan) for peptide map fingerprinting (PMF) in the case of bands 1 – 7, or by

liquid chromatography ion trap time-of-flight (LC-IT-TOF) for MS/MS ion search in the case of band 8 in Figure 5B. Matching peptides and proteins were run through a MASCOT analysis. The emPAI (exponentially modified protein abundance index) of each protein identified in band 8 was as follows: Histone A (8.46), Histone B (59.35), RNAP subunits N (1.34), K (0.58) and P (0.74), TK1040 (0.62) and TK1270 (0.54). The relative abundance of proteins in the band 8 (Figure 5B) was determined from the molecular weight and emPAI of each protein as described previously (Ishihama *et al.*, 2005). The amount of Histone A and Histone B together was estimated to be ~95% (weight) of total protein in the band 8 (~12% histone A and ~83% histone B) and the calculated amount of histone was adjusted accordingly.

2-8 Sucrose density gradient sedimentation of MNase-digested chromatin

Each chromatin fraction extracted from 30 – 60 ml of culture was digested with one unit of MNase (Worthington Biochemical) in 100 µl of MNase buffer for 30 min at 37°C in the presence of RNase A (10 µg/µl). The reaction was stopped by adding EDTA to 50 mM. Digested chromatin was applied to 5 ml of 5% - 20% sucrose density gradient in Sucrose gradient (SG) buffer (20 mM Tris-HCl (pH 7.4), 5 mM NaCl, 50 mM EDTA), made in 13 x 51 mm thinwall polyallomer or Ultra-Clear^{TM} tubes (Beckman Coulter, Brea, CA, USA) using the Gradient Master device (BioComp Instruments, Inc., Fredericton, NB, Canada). Centrifugation was performed at 28,000g for 16 - 24 hours at 4°C in a swinging-bucket MLS-50 rotor (Beckman). Ten fractions (500 µl each) were collected from the surface by means of careful pipetting. Extraction of DNA and protein from each fraction is described in Supplemental Materials. For AFM observation of chromosome fragments, 50µl of each fraction was passed through a Micro Bio-Spin Tris column (Bio-Rad) pre-equilibrated with SG buffer and applied onto a mica surface (pretreated with spermidine) at an appropriate concentration after fixation with 0.3% glutaraldehyde (for 30 min at 25°C).

2-9 Antibodies and western blotting

After SDS-PAGE, proteins were transferred to a PVDF membrane (Bio-Rad Laboratories, Hercules, CA, USA) and probed with rabbit antisera against chromosomal proteins. HRP-conjugated anti-rabbit secondary antibody (GE Healthcare, Chalfont St. Giles, UK) was used (1: 15,000 dilution). Primary antibodies used in this study were anti-Lon protease rabbit antiserum (Fukui *et al.*, 2002); anti-Histone B (HpkB), anti-Alba and anti-TK0471 rabbit antisera produced by Keari Co. Ltd. (Osaka, Japan). Signals were detected using both the ECL system (GE Healthcare) and the LAS-3000

system (Fujifilm).

2-10 Extraction of DNA and protein from fractions in sucrose density gradient sedimentation

Each fraction was separated into two for DNA and protein extraction. To extract DNA, each fraction was mixed with TNE buffer containing Proteinase K (100 μg/ml) and incubated for 1 hour 37°C. Following phenol extraction and ethanol precipitation, the pellet was dissolved in TE buffer and then treated with RNase A (5 μg/ml) and proteinase K (100 μg/ml). After precipitation with ethanol, DNA was dissolved in TE buffer. The protein in each fraction was concentrated by means of the general trichloroacetic acid (TCA) precipitation method, and was separated through SDS-PAGE and visualized by CBB staining.

2-11 Preparation of recombinant proteins

Plasmids for expression of *T. kodakarensis* Histone A (HpkA; TK1413) and Histone B (HpkB; TK2289) in *E. coli* were kindly provided by Dr. Higashibata and Dr. Fujiwara (Higashibata *et al.*, 1999). Genes encoding Alba (TK0560) and TK0471 were amplified by PCR using genomic DNA as a template and were inserted into pET vectors (Novagen, Madison, WI), with no additional amino acid sequence added to the native sequence. *E. coli* BL21-CodonPlus (DE3)-RIL competent cells (Stratagene, La Jolla, CA, USA) were transformed with these plasmids and were cultured to the log phase. Expression of the proteins was induced by the addition of IPTG to a concentration of 0.1 mM. The cells were harvested after 24 hours of culturing at 20°C.

HpkA (Histone A): *E. coli* cells expressing HpkA were resuspended in lysis buffer H (50mM Tris-HCl (pH 8.0), 100mM NaCl) and disrupted by sonication at 4°C. *E. coli* proteins were denatured by heat treatment (15 min at 80°C) and removed by centrifugation (15 min at 13,000 rpm at 4°C). Five millimolar $MgCl_2$ and 0.025U/μl DNase I (Takara Bio Inc.) were added, and the sample was incubated for 3 hours at 37°C. Fifty millimolar Tris-HCl (pH 8.0) and 3M NaCl were added to remove contaminating *E. coli* DNA from the protein. DNase I was denatured by a subsequent heat treatment (15 min at 80°C) and removed by centrifugation (20 min at 13,000 rpm at 4°C). Supernatant was dialyzed against 50mM Tris-HCl (pH 8.0) for 16 hours. The sample was loaded on a HiTrap SP column (GE Healthcare) pre-equilibrated with 50mM Tris-HCl (pH 8.0). HpkA was eluted in a linear gradient to 1M NaCl in 50mM Tris-HCl (pH 8.0).

HpkB (Histone B): *E. coli* cells expressing HpkB were resuspended in lysis

buffer H (50mM Tris-HCl (pH 8.0), 100mM NaCl) and disrupted by sonication at 4°C. *E. coli* proteins were denatured by heat treatment (15 min at 80°C) and removed by centrifugation (15 min at 13,000 rpm at 4°C). Five millimolar $MgCl_2$ and 0.025U/μl DNase I (Takara Bio Inc.) were added, and the sample was incubated for 3 hours at 37°C. Precipitate containing HpkB formed during this incubation. The precipitate was collected by centrifugation. Fifty millimolar Tris-HCl (pH 8.0) and 3M NaCl were added to dissolve the precipitate and to remove contaminating *E. coli* DNA from the protein. DNase I was denatured by a subsequent heat treatment (15 min at 80°C) and removed by centrifugation (20 min at 13,000 rpm at 4°C). Supernatant was dialyzed against 50mM Tris-HCl (pH 8.0) for 16 hours, resulting in the formation of HpkB precipitate. NaCl was added to 150mM to dissolve the precipitate. The sample was loaded on a HiTrap SP column (GE Healthcare) pre-equilibrated with 50mM Tris-HCl (pH 8.0) and 150 mM NaCl. HpkB was eluted in a linear gradient from 150mM to 1M NaCl in 50mM Tris-HCl (pH 8.0).

TK0471: *E. coli* cells expressing TK0471 were resuspended in lysis buffer T (50mM Tris-HCl (pH 6.8), 100mM NaCl) and disrupted by sonication at 4°C. *E. coli* proteins were denatured by heat treatment (15 min at 80°C) and removed by centrifugation (15 min at 13,000 rpm at 4°C). Five millimolar $MgCl_2$ and 0.025U/μl DNase I (Takara Bio Inc.) were added, and the sample was incubated for 3 hours at 37°C. Fifty millimolar Tris-HCl (pH 6.8) and 3M NaCl were added to remove contaminating *E. coli* DNA from the protein. DNase I was denatured by a subsequent heat treatment (15 min at 80°C) and removed by centrifugation (20 min at 13,000 rpm at 4°C). Supernatant was applied to PD-10 Desalting column (GE Healthcare) pre-equilibrated with 50mM Tris (pH 6.8) and 60mM NaCl. The sample was loaded on a HiTrap Q column (GE Healthcare) pre-equilibrated with 50mM Tris-HCl (pH 6.8). TK0471 was eluted in a linear gradient to 1M NaCl in 50mM Tris-HCl (pH 6.8). Peaks containing TK0471 were pooled and the sample was then separated on Superdex 75 or Superdex 200 columns (GE Healthcare) pre-equilibrated with 50mM Tris-HCl (pH6.8) and 300mM NaCl. Peak fractions containing TK0471 protein was collected.

Alba: *E. coli* cells expressing Alba were resuspended in lysis buffer A (50mM Tris-HCl (pH 7.5), 150mM NaCl) and disrupted by sonication at 4°C. *E. coli* proteins were denatured by heat treatment (15 min at 80°C) and removed by centrifugation (15 min at 13,000 rpm at 4°C). The sample was loaded on a HiTrap SP column (GE Healthcare) pre-equilibrated with 50mM Tris-HCl (pH 7.5). Alba was eluted in a linear gradient from 150mM to 1M NaCl in 50mM Tris-HCl (pH 7.5).

2-12 Reconstitution of chromatin structures using recombinant proteins

For *in vitro* reconstitution, pBluescript II (Stratagene) plasmid was digested by the ion enzyme HindIII. The linear DNA was mixed with each recombinant protein (in 10 mM Tris (pH 8.0), 200 mM NaCl) in a DNA: protein ratio (wt: wt) of 1: 0, 1: 0.3, 1: 1, 1: 3 or 1: 10 and incubated for 20 min at 50°C. In the electrophoretic mobility shift assay, the protein-DNA complexes were run through 0.8% agarose gel in 1x TAE buffer. For AFM observation, the protein-DNA complexes were diluted to 1: 20 in AFM fixation buffer (10 mM Tris (pH 8.0), 5 mM NaCl, 0.3% glutaraldehyde). After incubation for 30 min at 25 °C, 10 µl of the mixture (equivalent to ~2.5 ng of DNA) was deposited on mica that had been pretreated with 10 mM spermidine for 10 min. After 10 min of incubation, the mica was washed with 1 ml of pure water and dried with nitrogen gas. AFM observation and analysis was performed as described above.

2-13 DNA sequencing

DNA in the light fraction (third fraction from the top) and the heavy fraction (eighth fraction) in the 5% - 20% sucrose density gradient sedimentation of MNase-digested chromatin fraction of the KOD1 strain in the log phase was purified through phenol/chloroform extraction and ethanol precipitation, following RNase A and Proteinase K treatment of each fraction. Purified DNA was sequenced using a SOLiD 3 sequencer (Applied Biosystems, Foster City, CA, USA). Purified KOD1 genomic DNA was also sequenced as a control. “Fold enrichment” value was determined by dividing the degree of sequence enrichment in the sample with the degree of enrichment in the control sample. Peaks were defined as the middle nucleotide positions of genomic regions enriched more than twofold in a particular fraction. DNA in the light and heavy fractions in the stationary phase was purified, treated with DNA Polymerase I Klenow fragment (New England Biolabs, Ipswich, MA, USA), cloned into a plasmid pBluescript II (Stratagene), and then sequenced with Sanger method. Peaks were defined as the middle nucleotide positions of the cloned regions. The UCSC Archaeal genome Browser (http://archaea.ucsc.edu/) was used in part to analyze the data (Schneider *et al.*, 2006).

2-14 Microarray analysis

T. kodakarensis KUW1 (wild type) and KCP1 (*ΔTK0471*) strains were cultivated at 85°C in ASW-YT-S^0 media. Cells were harvested in the early log phase (O.D.660 = 0.1) and total RNA was extracted using the RNeasy Midi kit (Qiagen, Hilden, Germany). The microarray plate used in this study (Array Tko2) was manufactured at Takara Bio

(Otsu, Japan) and covers all 2306 ORFs that have been predicted to exist in the *T. kodakarensis* genome. DNA fragments about 300 bp in length, corresponding to the 3′ -terminal regions of each coding region, were spotted on the glass plate. Because two identical sets (left and right) were loaded onto each plate, two sets of data were obtained from each microarray plate. Average signal ratios and standard deviations are shown in the data files. Java TreeView was used to visualize the microarray data (Saldanha, 2004).

2-15 Statistical analysis

Analyses were performed using the statistical package R (http://www.r-project.org/) (R Development Core Team, 2010).

To evaluate the degree of overlap between the DNA sequences that were concentrated in each of the various fractions in the sucrose density gradient sedimentation experiment, a bimodal test with a Bonferroni correction was performed. In the log phase, the rate of overlap in nucleotide positions between the histone-rich light and TK0471-rich heavy fractions (7.3%) was significantly lower than the rate that would have been expected from a random distribution of the same number of nucleotide positions (7.7%) ($P = 0.0015$).

The nucleotide positions between the genomic regions that were concentrated in the light fraction in the stationary phase had a significantly lower rate of overlap (2.5%) with the light fraction in the log phase ($P < 1.3E-15$), but a significantly higher rate of overlap (9.9%) with the region that was concentrated in the heavy fraction in the log phase ($P < 1.3E-15$), compared to what would have been expected from random distributions (3.8% and 7.7%, respectively) of the same numbers of nucleotide positions (binomial test with Bonferroni correction).

The same statistical tests were used to evaluate the degree of overlap among the DNA sequences present in high concentrations in the various sucrose fractions in the log and the stationary phases. The rate of overlapping nucleotide positions between the genomic regions that were concentrated in the heavy fraction in the stationary phase and those that were concentrated in the histone-rich fraction in the log phase (7.5%), or those that were concentrated in the region enriched in the heavy fraction in the log phase (13.7%), were significantly higher than would have been expected from random distributions of the same numbers of nucleotide positions (3.8% and 7.7% respectively; $P < 1.3E-15$ in both cases, binomial test with Bonferroni correction).

3. Results

3-1 *T. kodakarensis* chromosome consists of beads-on-a-string structures and fibrous structures

Hypotonic treatment of *T. kodakarensis* KOD1 cells attached to a cover glass can disrupt the cell membrane and release the chromosome fibers from the cells. The chromosome fibers exposed from the cells in the log and stationary phases were visualized by staining DNA with 4',6-diamino-2-phenylindole (DAPI). The degree of chromosome spreading was greater in the cells from the log phase culture than in those from the stationary phase (Figure 3). Detailed results were obtained through structural analysis by atomic force microscopy (AFM) (Figure 4A). Chromosome fibers released from the cells in the log phase exhibited both a beads-on-a-string structure and fibrous structures in the regions where the chromosome fibers were well spread. The diameter of the "bead" was 8.7 ± 1.1 nm (mean ± standard deviation (SD), n = 150) (Figure 4B). This size was similar to that of archaeal nucleosomes isolated from the chromosome or reconstituted with recombinant histone protein (see below). The diameter of the fibers had a broader distribution (15.5 ± 5.0 nm, n = 85) (Figure 4C). Although some portion of the thick fibers could have resulted from bundling of chromosome fibers released upon cell lysis, these results indicate the existence of heterogeneous structural elements in the *T. kodakarensis* chromosome. As shown below, histone, Alba and TK0471/TrmBL2 are the major DNA-binding proteins on the *T. kodakarensis* chromosome that create different structures on DNA. The fact that similar structures were observed in the chromosome fibers released from the cell, as well as in isolated or reconstituted chromatin, supports the existence of these structures in the cell.

Consistent with the fluorescent imaging result was the observation that the chromosome released from cells in the stationary phase appeared in a condensed form under AFM. Individual fibrous structures could not be detected from condensed stationary phase chromosomes (Figure 3).

3-2 A putative helix-turn-helix protein is one of the major chromosomal proteins in *T. kodakarensis*

Cell-free extract of *T. kodakarensis* was prepared through gentle treatment of the cells with a detergent, followed by a low-speed centrifugation through sorbitol (Matsunaga *et al.*, 2001). Chromatin was isolated as an insoluble pellet (hereafter referred to as the "chromatin fraction"). Separation of the protein component of the chromatin fraction through SDS-PAGE followed by Coomassie staining resulted in 20 to 30 visible bands,

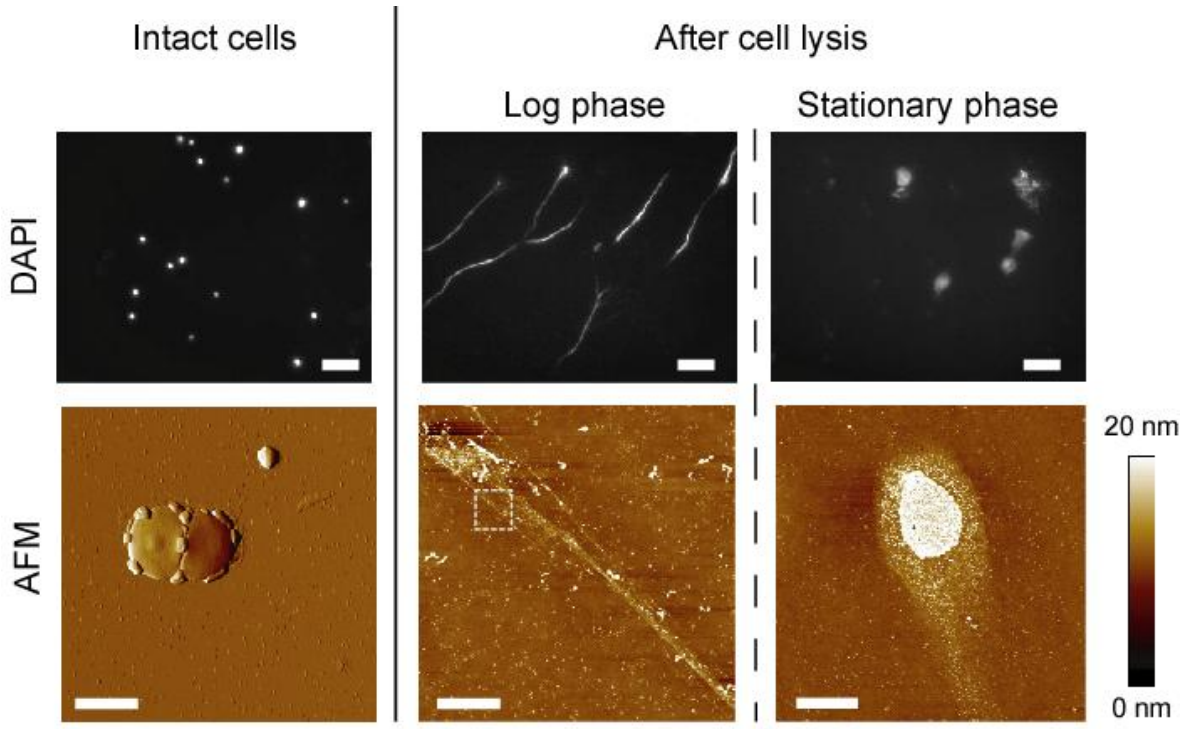

Figure 3

Figure 3. On-substrate-lysis of *T. kodakarensis* cell

DAPI staining (top; scale bars, 10 μm) and AFM images (bottom; scale bars, 2 μm) of chromosomes released from *T. kodakarensis* cells in the log and stationary phases. Intact cells are shown on the left.

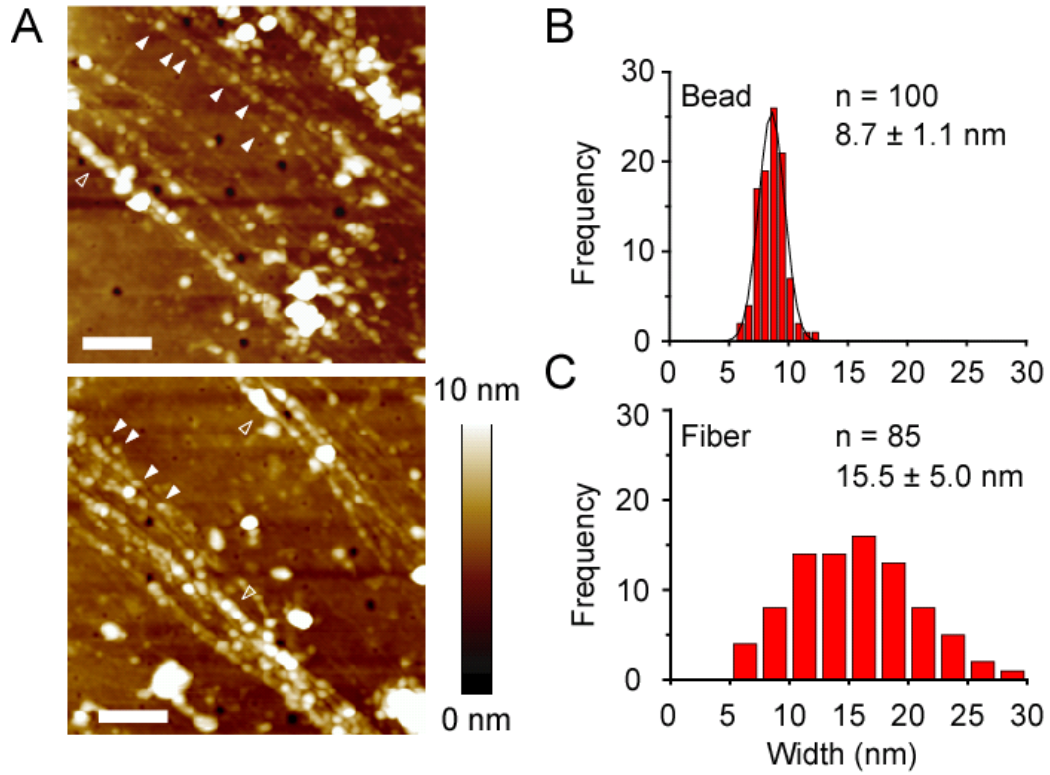

Figure 4

Figure 4. Chromosome fiber of *T. kodakarensis* analyzed through AFM

(A) Detailed AFM analysis of the chromosome fiber. Beads-on-a-string structures (solid triangles) as well as thick structures (open triangles) were observed in areas where chromosomes were well spread out [boxed area in Figure 3]. Scale bars, 200 nm. Histograms indicate the diameters of (B) beads and (C) fibrous structures. The means ± SD of the distributions are indicated. The curve indicates the fitted Gaussian function.

ranging from 6 kDa to 120 kDa in size (Figure 5, A and B). The chromatin fraction exhibited a pattern of proteins different from that exhibited by the whole cell lysate (Figure 5A). In addition, western blotting experiments showed that membrane-bound Lon protease (Lon_{Tk}) (Fukui *et al.*, 2002) was not present in the chromatin fraction (Figure 5A), indicating that the chromatin fraction was not contaminated with cell membrane or membrane-bound proteins. The fact that the chromosomes could easily be isolated indicates an important difference between the *T. kodakarensis* chromosomes and the *E. coli* nucleoid, which cannot be separated from the cell membrane (Zimmerman, 2006). There was a slight difference in protein composition between the chromatin fractions taken from cells in the log phase and the stationary phase (Figure 5B).

Protein bands of high intensity in the chromatin fraction of the KOD1 strain in the stationary phase were excised from the gel and analyzed through mass spectrometry. The identified proteins include DNA-binding proteins such as Histone A, Histone B, Alba, TK0471 and RNA Polymerase (RNAP) subunits A', A'', B, N, K and P (Figure 5B). Micrococcal nuclease (MNase) digestion of the chromatin fraction resulted in a laddered pattern of DNA (~60, 90, 120, 150 bp etc.) indicating the presence of a nucleosome structure *in vivo* (Figure 5C). Among the bands of DNA-binding proteins, the ~6 kDa band, which contains histones, had the highest intensity, but that of the ~32 kDa band was also high; the ~32 kDa band contains TK0471, a protein which has a putative helix-turn-helix (HTH) DNA-binding motif at the N-terminus.

The molecular ratio of Alba and TK0471 relative to histone was estimated to be 0.19 ± 0.06 and 0.10 ± 0.02 respectively, by dividing the intensity of each band in SDS-PAGE by the molecular weight of each protein (Figure 5, D and E). In addition to these DNA-binding proteins, proteins without an obvious DNA-binding function were identified (see Figure 5B caption).

3-3 Each chromosomal protein forms a different structure on double-stranded DNA

The chromatin fraction of the *T. kodakarensis* strain KOD1 was partially digested with MNase, then subjected to 5% - 20% sucrose density gradient sedimentation, in the expectation that the various structural elements would be separated according to their protein components and densities. Histones were concentrated in low- to middle-density sucrose fractions. TK0471 was concentrated in middle- to high-density fractions, and RNAP subunits were concentrated in middle-density fractions; this was observed through SDS-PAGE followed by Coomassie staining and western blotting (Figure 6A).

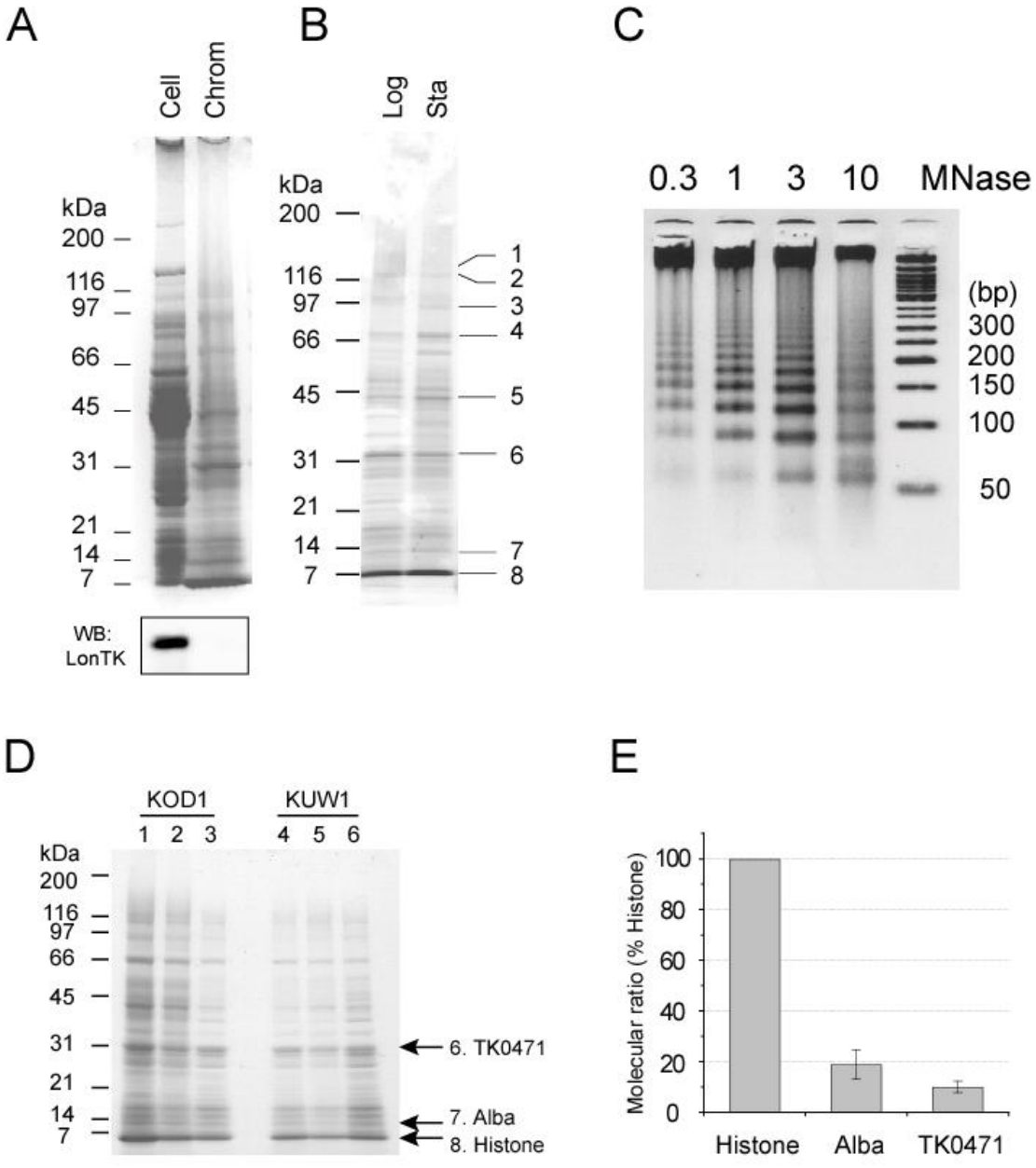
A
Cell
Chrom
kDa
200
116
97
66
45
31
21
14
7
WB:
LonTK
B
Log
Sta
kDa
200
116
97
66
45
31
21
14
7
1
2
3
4
5
6
7
8
C
0.3
1
3
10
MNase
(bp)
300
200
150
100
50
D
KOD1
KUW1
1 2 3
4 5 6
kDa
200
116
97
66
45
31
21
14
7
6. TK0471
7. Alba
8. Histone
E
Molecular ratio (% Histone)
100
80
60
40
20
0
Histone
Alba
TK0471

Figure 5

Figure 5. Protein component of *T. kodakarensis* chromosome

(A) Protein components of whole cell ("Cell") and of the chromatin fraction ("Chrom") of the KOD1 strain. Western blotting with an antiserum against the membrane-bound protease Lon_{TK} is shown at the bottom. (B) Protein components of chromatin fractions of KOD1 in the log and stationary phases. The protein bands analyzed through mass spectrometry are numbered on the right. The identified proteins were 1) Predicted endonuclease-methyltransferase fusion protein (TK1460), 2) RNA Polymerase (RNAP) subunit B (TK1083), 3) RNAP subunit A' (TK1082), 4) Acylamino acid-releasing enzyme (TK0752), 5) RNAP subunit A'' (TK1081) and glutamate dehydrogenase (TK1431), 6) TrmBL2 (TK0471) and fluctose-bisphosphate aldolase (TK0989), 7) Alba (TK0560), 8) Histone A (TK1413), Histone B (TK2289), RPAP subunit N (TK1499), K (TK1498) and P (TK0616), hypothetical proteins TK1040 and TK1270. Histones were estimated to constitute ~ 95% of the band 8. (C) Chromatin fraction of KOD1 was mildly digested with increasing amounts of MNase (0.3, 1, 3 and 10 units/μl) and separated on 4% NuSieve GTG agarose gel in 1x TBE. (D) Chromatin fractions taken from independent cultures of wild types KOD1 (lane1 - 3) and KUW1 (lane 4 – 6) were separated through SDS-PAGE. (E) Molecular ratio of histone, Alba and TK0471 was calculated by dividing the signal intensity of the bands by the molecular weight of each protein. Average of 7 independent results (6 shown in (A) and one in Figure 4B) are shown (Mean ± SD).

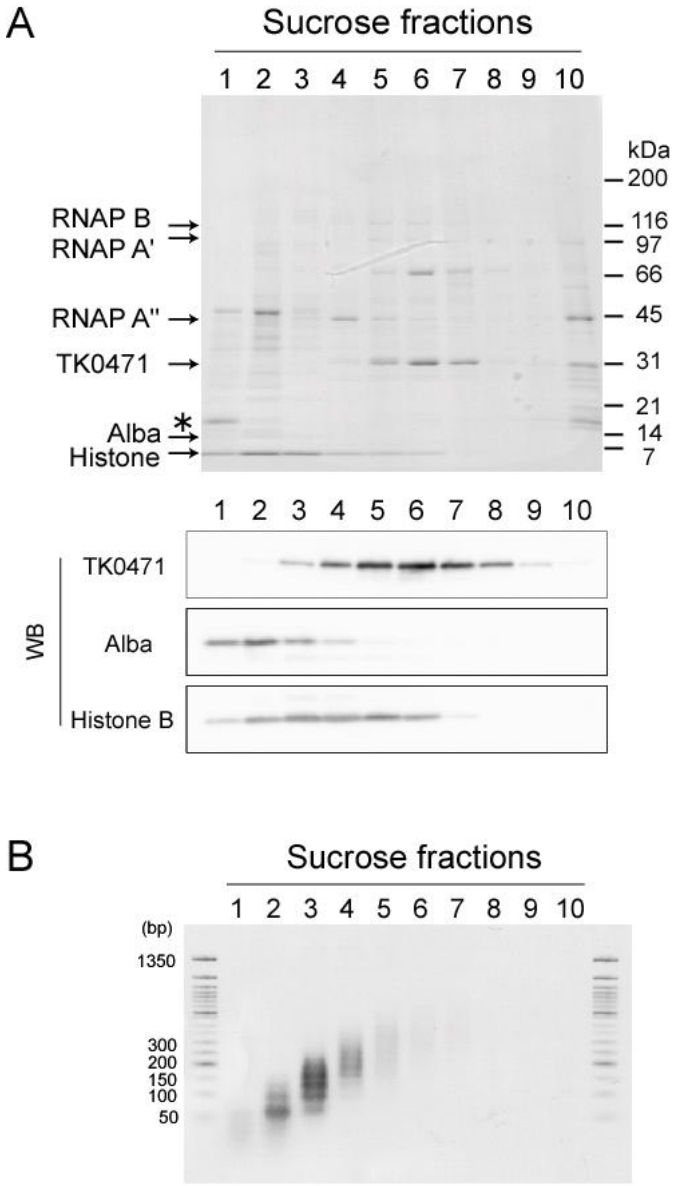

Figure 6

Figure 6. Separation of chromosome fragments with different protein components
(A) MNase-digested KOD1 chromatin fraction taken from stationary phase cells was separated through 5% – 20% sucrose density gradient sedimentation. The protein in each fraction was concentrated by means of trichloroacetic acid precipitation and separated on 5% - 20% SDS-polyacrylamide gel. The positions of known protein bands are indicated. The asterisk indicates RNase A. Western blotting with antisera against TK0471, Alba or Histone B is shown at the bottom. (B) DNA was extracted and separated on 2.5% agarose gel in 0.5x TBE buffer.

The distribution of Alba was observed in low-density fractions, partially overlapping with the distribution of histone (Figure 6A).

The length of the DNA that was abundant in each fraction was determined through agarose gel electrophoresis (Figure 6B). The light fractions were enriched with small DNA fragments (60-300 bp). A characteristic laddered pattern (~60, 90, 120 bp etc.) was observed in the light fractions, implying that the nucleosome structures were abundant in these fractions (Bailey *et al.*, 2000). The TK0471-rich heavy fractions were enriched with longer DNA fragments (200-1000 bp), although much less DNA was present in this fraction than in the lighter fractions (Figure 6B).

The structures of the chromosome fragments that accumulated in the light and heavy fractions were analyzed through AFM. Chromosome fragments in the light fraction (fraction 3) exhibited mainly a beads-on-a-string structure. The diameter of the beads was 8.6 ± 1.8 nm (mean ± SD, n = 100) (Figure 7A). On the basis of this observation, as well as on the histone accumulation and the laddered pattern of the DNA in this fraction (Figure 6, A and B), we concluded that the light fraction contains a high concentration of the archaeal nucleosome structure. In contrast, the heavy fraction (fraction 8) contained mainly chromosome fragments in a thick fibrous structure, the diameter of which was 13.1 ± 2.2 nm (mean ± SD, n = 100) (Figure 7B). Both the beads-on-a-string structure and the fibrous structure were detected in both the log phase and the stationary phase in KUW1, another wild type strain (see below and Figure 11A).

Next, we tested the ability of histone, Alba and TK0471 proteins to reconstitute different structures *in vitro*. Recombinant Histone A (HpkA), Alba or TK0471 proteins were expressed in *E. coli* and purified (see Figure 8P). Incubation of each protein with a linear 3-kbp DNA altered the mobility of the DNA through an agarose gel (Figure 8, A - C). The structures of the resulting DNA-protein complexes were examined through AFM (Figure 8, D – G). The diameter and contour length of the 3-kbp dsDNA molecule used in this experiment were 1.83 ± 0.37 nm (n = 100) and 1003 ± 30 nm (mean ± SD, n = 100), respectively (Figure 8, H and L), which correspond to the theoretical diameter (2 nm) and the length (0.34 nm/bp) of B-form DNA. Beads-on-a-string structures were formed when Histone A (HpkA) was mixed with linear 3-kbp DNA (Figure 8E). The diameter of the beads was 8.9 ± 1.5 nm (n = 150) (Figure 8I). The contour length of the histone-bound DNA was 607 ± 74 nm (n = 100) (Figure 8M), significantly shorter than that of the naked DNA ($P < 0.01$, Tukey's HSD test). Taking into account the number of nucleosomes formed on each DNA molecule (10.1 ± 1.5, n = 54), I concluded that 113 ± 16 bp (38.6 ± 5.3 nm, n = 54) of DNA were incorporated into a single nucleosome on average. Incubation of TK0471 with DNA gave the genetic material a thick fibrous

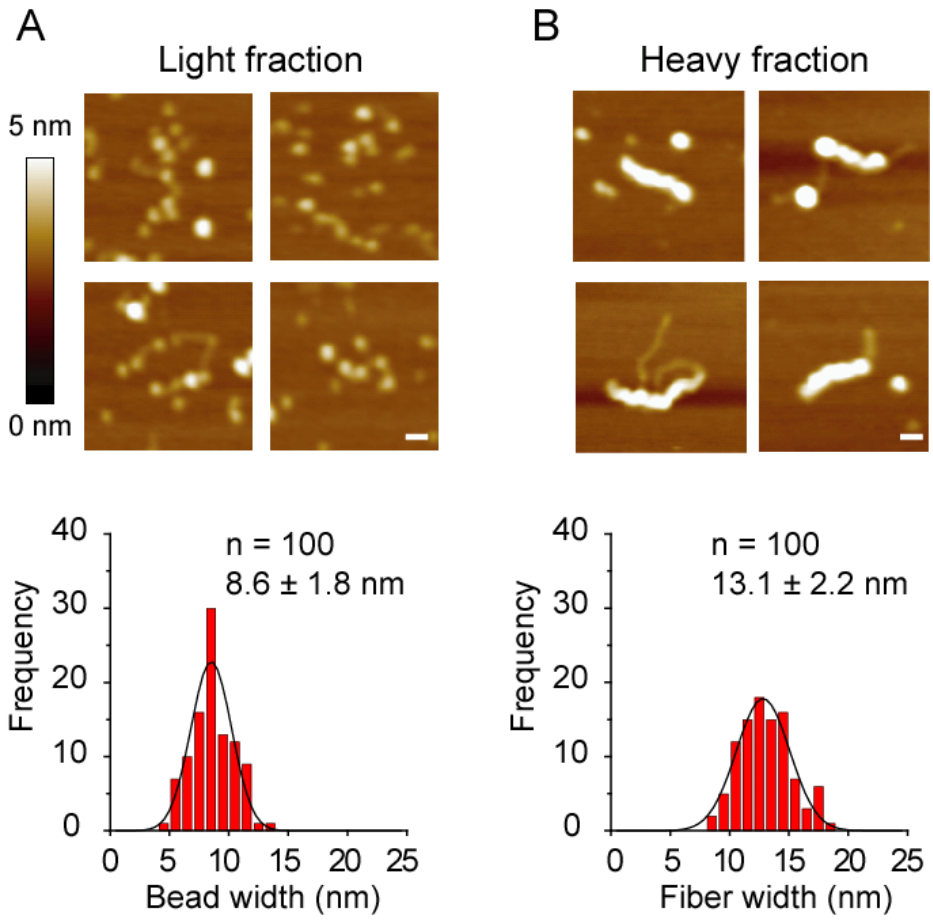

Figure 7

Figure 7. AFM analysis of different chromosome fragments

Chromosome fragments in (A) the light fraction (fraction 3) and (B) the heavy fraction (fraction 8) (B). Scale bars, 50 nm. Histograms below the images indicate the diameter of each structure. The means ± SD of the distributions are indicated. The curves indicate the fitted Gaussian functions.

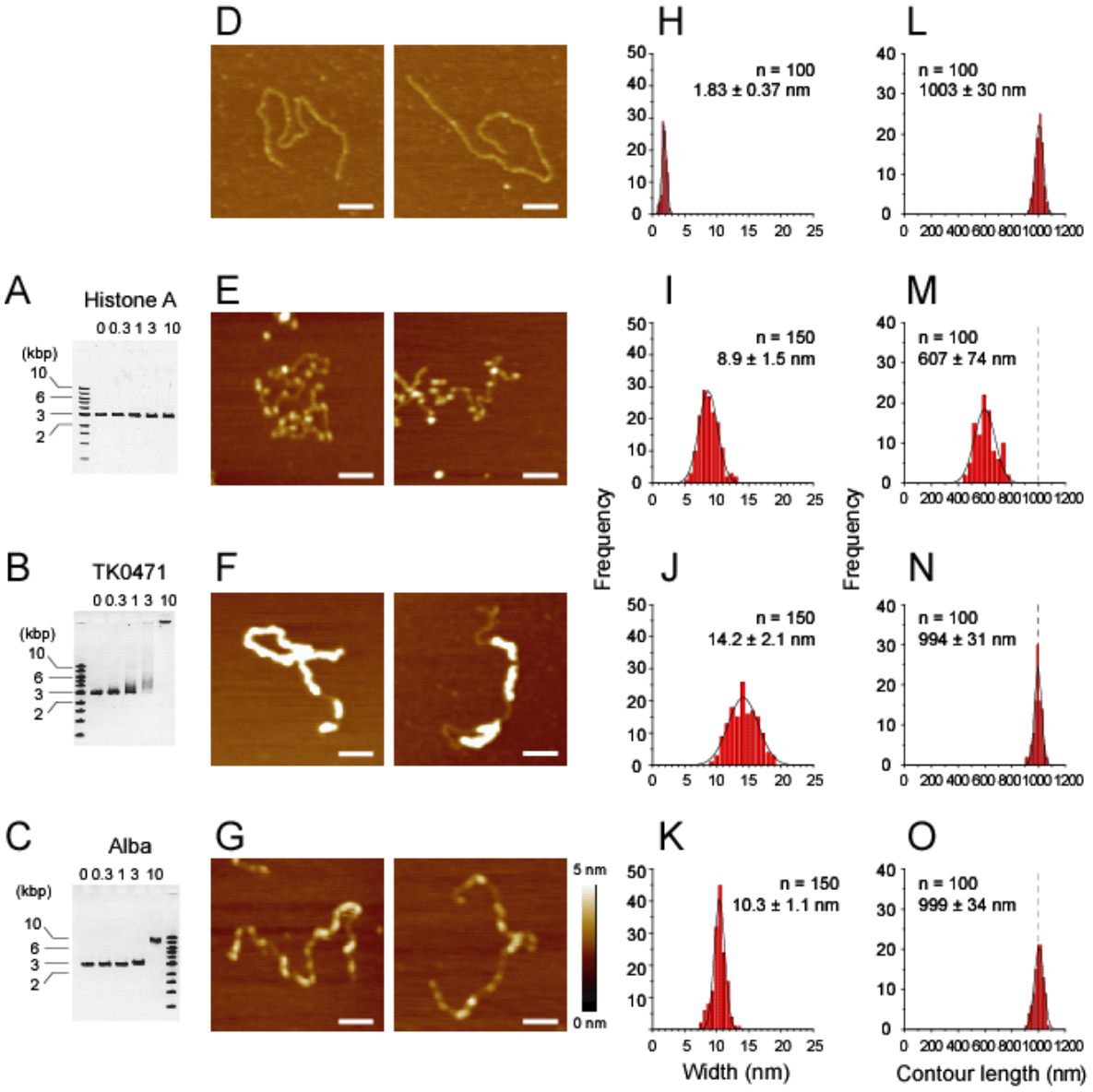
A
Histone A
0 0.3 1 3 10
(kbp)
10
6
3
2
B
TK0471
0 0.3 1 3 10
(kbp)
10
6
3
2
C
Alba
0 0.3 1 3 10
(kbp)
10
6
3
2
D
E
F
G
5 nm
0 nm
H
n = 100
1.83 ± 0.37 nm
I
n = 150
8.9 ± 1.5 nm
J
n = 150
14.2 ± 2.1 nm
K
n = 150
10.3 ± 1.1 nm
Width (nm)
L
n = 100
1003 ± 30 nm
M
n = 100
607 ± 74 nm
N
n = 100
994 ± 31 nm
O
n = 100
999 ± 34 nm
Contour length (nm)
Frequency
Frequency

Figure 8

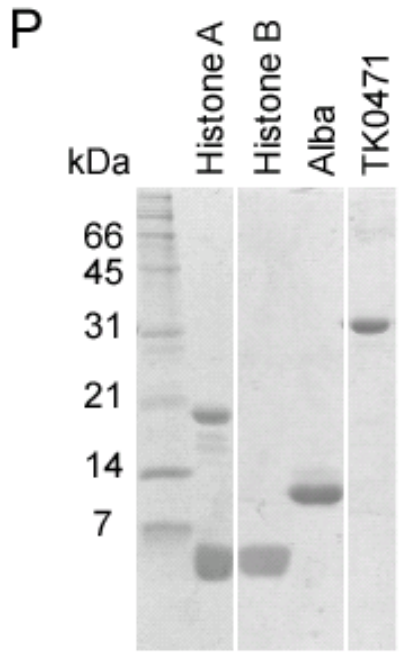

Figure 8

Figure 8. Recombinant chromatin proteins form distinct structures on dsDNA *in vitro*

(A-C) Mobility shift of DNA upon binding of recombinant chromatin proteins. One hundred nanograms of linear 3-kbp DNA (pBluescript II) was incubated with (A) Histone A, (B) TK0471 or (C) Alba and separated through 0.8% agarose gel electrophoresis in 1x TAE. The protein/DNA ratio (wt/wt) was 0, 0.3, 1, 3, or 10 as indicated in each lane. (D-G) AFM images of (D) 3-kbp linear DNA, (E) 3-kbp linear DNA incubated with recombinant Histone A, (F) TK0471 or (G) Alba at a protein-to-DNA ratio of 10: 1 (wt/wt). Scale bars, 100 nm. (H-K) Diameters of (H) naked dsDNA and those of the structures formed in the DNA by (I) Histone A, (J) TK0471 and (K) Alba are shown in histograms. (L-O) Contour length of the 3-kbp DNA molecule without protein (L) and lengths of the molecule when bound with recombinant (M) Histone A, (N) TK0471 and (O) Alba are indicated in histograms. The means ± SD of the distributions are indicated. The curves indicate the fitted Gaussian functions. (P) Purified recombinant proteins were analyzed through SDS-PAGE and Coomassie staining. ~20kDa protein in Histone A preparation might be a stable histone tetramer. Histone B was used as an antigen for producing antibodies.

structure (Figure 8F) with a diameter of 14.2 ± 2.1 nm (n = 150) (Figure 8J), similar to that of the fibers observed in the TK0471-rich heavy fractions (Figure 7B). Incubation of Alba with DNA gave the genetic material a fibrous structure with a diameter of 10.3 ± 1.1 nm (n = 150) (Figure 8, G and K), thinner than that of the fibers formed in the presence of TK0471. The individual fibrous structure made with Alba, but not the contour DNA length, was shorter compared to that made with TK0471 (Figure 8, F and G). In contrast to histone, neither TK0471 (994 ± 31 nm, n = 100) nor Alba (999 ± 34 nm, n = 100) significantly reduced DNA contour length (P = 0.52 and 0.92 respectively, Tukey's HSD test) (Figure 8, N and O).

3-4 Histone and TK0471 localize to both coding and non-coding regions

Localization of each chromosomal structure on the genome was determined through massively parallel sequencing of DNA accumulated in the light and the heavy fractions in the log phase. Fraction 3 was chosen as the histone-rich light fraction. Although in the light fractions, the distribution of Alba and histone overlap I expect the majority of DNA in this fraction to represent histone-bound DNA, based on the relative abundance of histone and the laddered pattern of DNA characteristic of nucleosome formation (Figure 6, A and B). Fraction 8 was chosen as the TK0471-rich heavy fraction. The complete profiles of the entire genomic regions that were concentrated in each fraction are shown in Appendix A, and the nucleotide positions of the genomic sequences that were present at more than twice their normal concentration in each fraction are listed in Appendix B.

Peaks corresponding to the genomic regions that were concentrated in the light and heavy fractions were located throughout the genome and encompassed both coding and intergenic regions (Figure 9A). Among the 397 genomic regions that were concentrated more than twofold in the light fraction, 379 (95.5%) were located within the coding regions (ORFs and RNA coding genes) and 18 (4.5%) were located in the intergenic regions. Among the 449 genomic regions that were concentrated more than twofold in the heavy fraction, 407 (90.6%) were located within the coding regions and 42 (9.4%) were located in the intergenic regions. Ninety-two percent of the *T. kodakarensis* genome has been predicted to consist of coding regions (Fukui *et al.*, 2005). The distributions of the peaks in each fraction were not significantly biased toward the coding or intergenic parts of the genome compared to a random distribution of peaks along the genome. In addition, the distribution of peaks in the two fractions were not significantly different from each other (light fraction versus random distribution on the genome, P = 0.028; heavy fraction versus random distribution on the

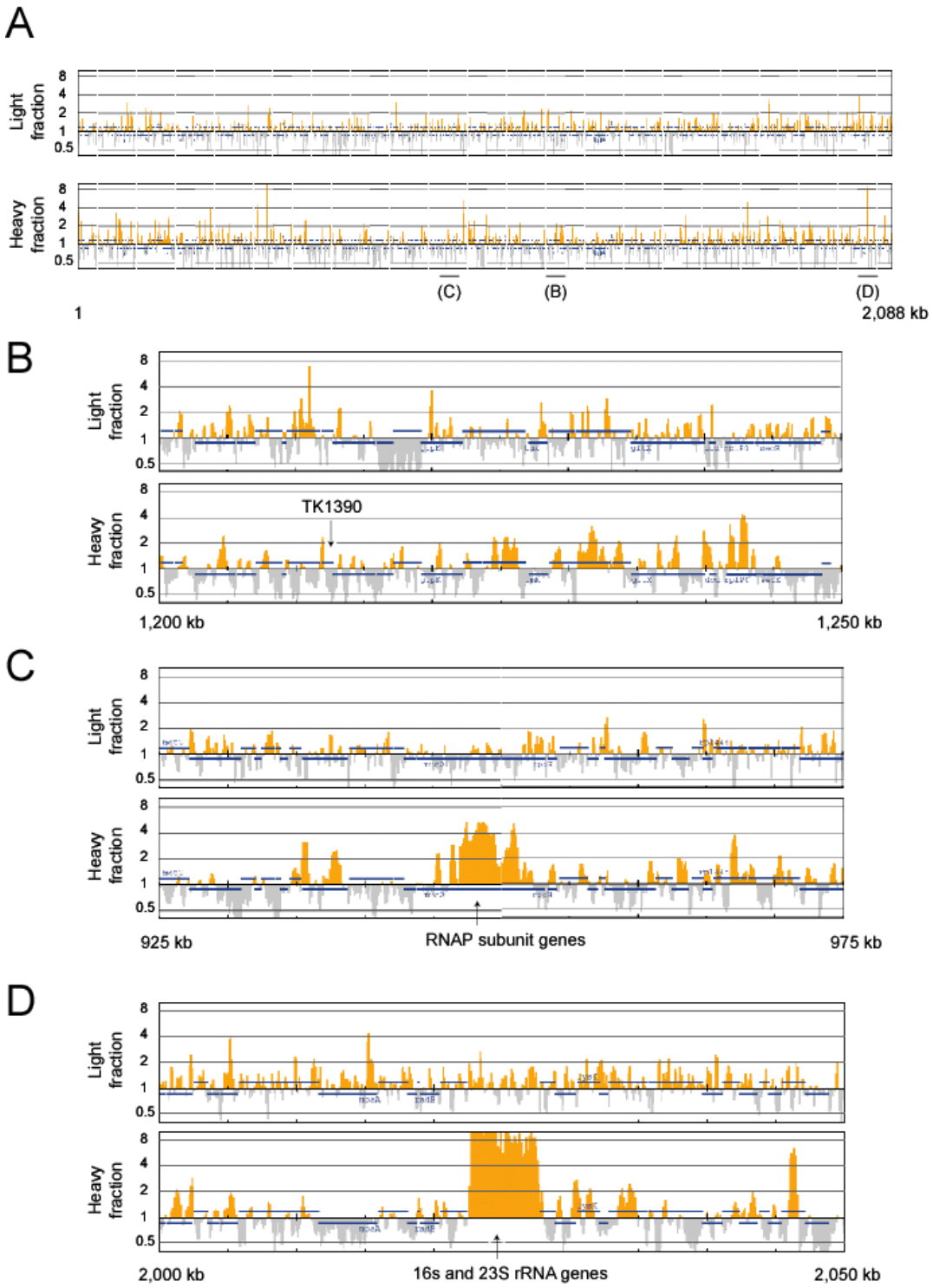
A
Light fraction
Heavy fraction
8
4
2
1
0.5
(C)
(B)
(D)
1
2,088 kb
B
TK1390
1,200 kb
1,250 kb
C
925 kb
RNAP subunit genes
975 kb
D
2,000 kb
16s and 23S rRNA genes
2,050 kb

Figure 9

Figure 9. Profiles of the DNA regions found at high concentrations in the light and heavy fractions

The x-axis indicates position on the genome. The blue bars above and below the baseline indicate predicted ORFs on the plus and minus strands, respectively. Note that a single bar can contain multiple overlapping ORFs. The y-axis indicates fold enrichment value of each sequence compared to that of the genomic DNA control. In each case, the profile of the light fraction (fraction 3) is shown in the top panel, and that of the heavy fraction (fraction 8) in the bottom panel. (A) Whole genome profile of the sequences highly concentrated in the light and heavy fractions. (B-D) Magnified profile of the genomic region including (B) the TK1390 gene, (C) RNAP subunit genes, and (D) 16S and 23S rRNA genes. See also Appendices A and B.

genome, $P = 0.772$; light fraction versus heavy fraction, $P = 0.021$; Fisher's exact test with Bonferroni correction).

Statistical analysis indicates that nucleosomes and TK0471 fibers tend not to colocalize in the log phase (see Materials and Methods). As an example, a profile of the DNA sequences that were concentrated in the light and heavy fractions in a 50-kb region including both intergenic and coding regions is shown in Figure 9B. Genomic sequences corresponding to the genes encoding DNA-directed RNA polymerase subunits A'' (TK1081), A' (TK1082) and B (TK1083) (Figure 9C) as well as 16S and 23S ribosomal RNA genes (Tkr05 and Tkr06) (Figure 9D) were particularly highly concentrated in the TK0471-rich heavy fraction.

The DNA sequence accumulated in the light and the heavy fractions in the stationary phase was also determined. In this case, DNA in each fraction was purified and cloned into a plasmid vector, then subjected to conventional Sanger sequencing. The entire list of genomic regions cloned from each fraction is shown in Appendix B. Statistical analysis indicates that the sequence of DNA in the light fraction tends to differ in the log and stationary phases, but that some portion of the DNA in the heavy fraction stays at the same position in both the log and stationary phases (See Materials and Methods for details).

3-5 Deletion of TK0471 gene leads to a loss of thick fibrous structure

A deletion strain of the TK0471 gene was constructed using a gene deletion system previously developed for this organism (Sato *et al.*, 2003). *T. kodakarensis* KUW1 strain (*ΔpyrF, ΔtrpE*) was used as the host strain to allow the use of the *pyrF* gene as a selectable marker (Figure 10A). KUW1 did not differ from KOD1 in terms of growth characteristics, protein composition in the chromatin fraction or chromosome fiber structure. Successful deletion of the TK0471 gene was confirmed through PCR and Southern blotting (Figure 10B), and the deletion strain (*ΔpyrF, ΔtrpE, ΔTK0471*) was designated KCP1. The KCP1 strain exhibited a slight growth delay compared to KUW1 (Figure 10C). When the chromatin fraction of KCP1 in the log phase was subjected to MNase digestion and sucrose density gradient sedimentation, the fibrous structures observed in the heavy fraction in wild-type KOD1 or KUW1 strains were not detected in any of the fractions (Figures 7B and 11A), supporting the conclusion that TK0471 is the protein component of these thick fibrous structures. Chromosome condensation was observed in the KCP1 strain in the stationary phase, as in the wild-type KOD1 and KUW1 strains (Figure 3 and 11B), indicating that TK0471 is not essential for condensation.

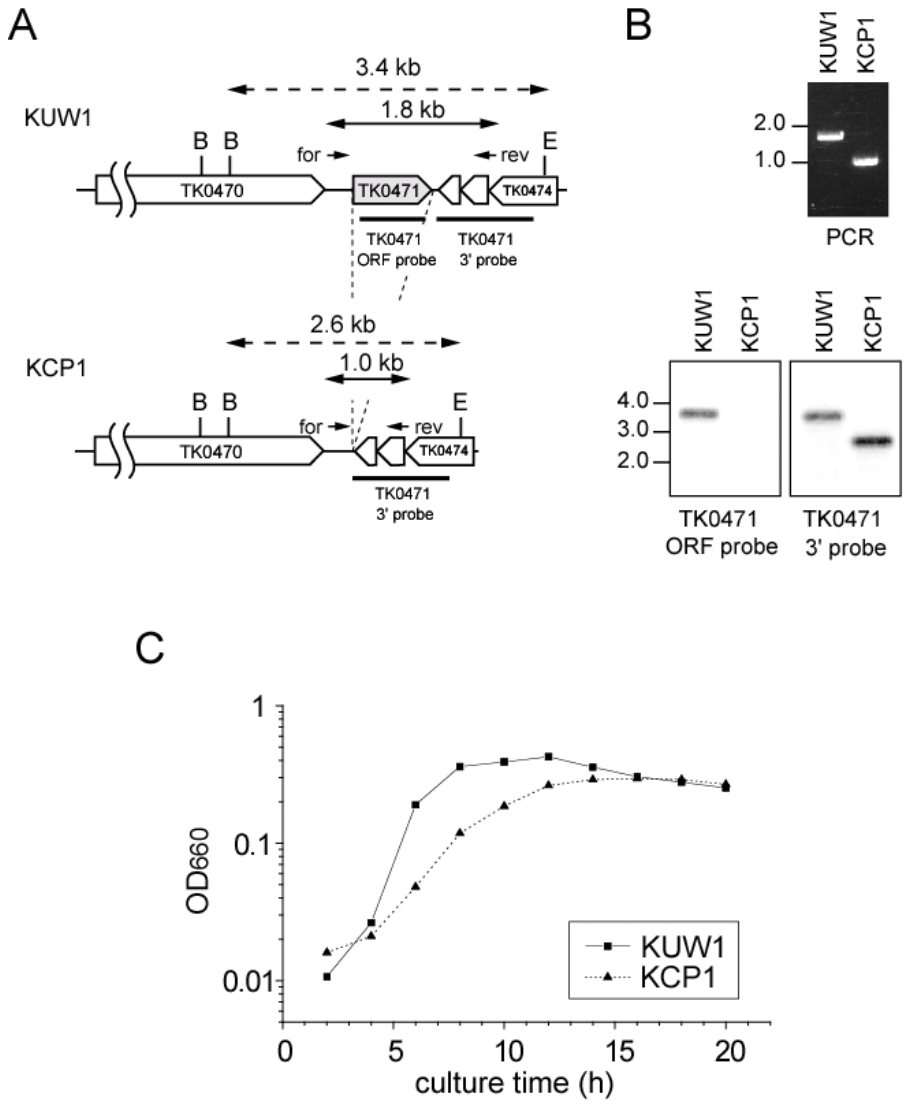

Figure 10

Figure 10. Construction of the ΔTK0471 strain

(A) Genome structure of KUW1 (wild type) and KCP1 (ΔTK0471) strains. B, BamHI; E, EcoRI site. PCR primers (arrows) and probes for Southern blotting (thick lines), as well as the distances between the PCR primers (solid lines) and the lengths of the restriction fragments (dashed lines) are indicated. (B) PCR and genomic Southern blotting were used to confirm the deletion of the TK0471 gene. (C) Growth characteristics of KUW1 (solid line) and KCP1 (dotted line) strains grown at 85°C in ASW-YT-S^0 medium.

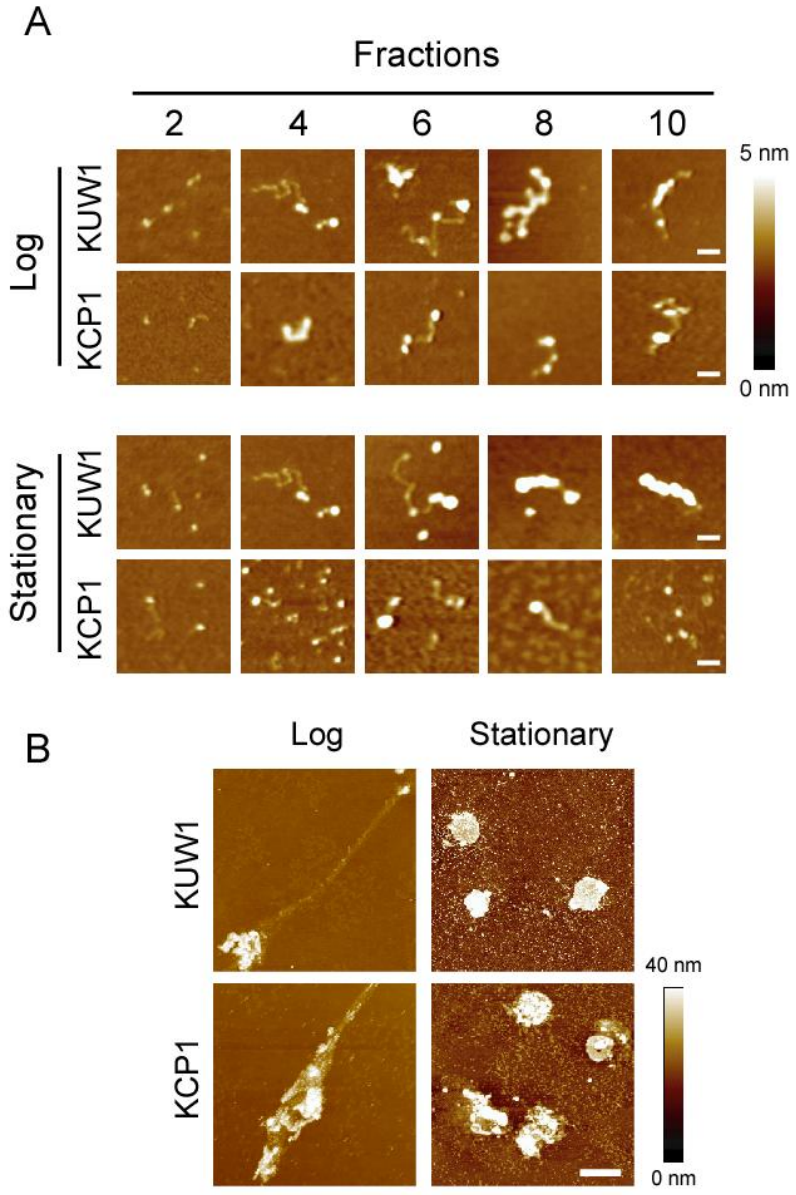

Figure 11

Figure 11. Analysis of the chromosome structure of the ΔTK0471 strain

(A) MNase-digested chromatin fractions of KUW1 and KCP1 strain (each in both log phase and stationary phase) were separated through 5% – 20% sucrose density gradient sedimentation. The thick fibrous structures that are characteristic of TK0471 were not observed in the KCP1 strain. Scale bars, 50 nm. (B) Chromosome condensation in the stationary phase occurs in the KCP1 strain. Scale bar, 2 μm.

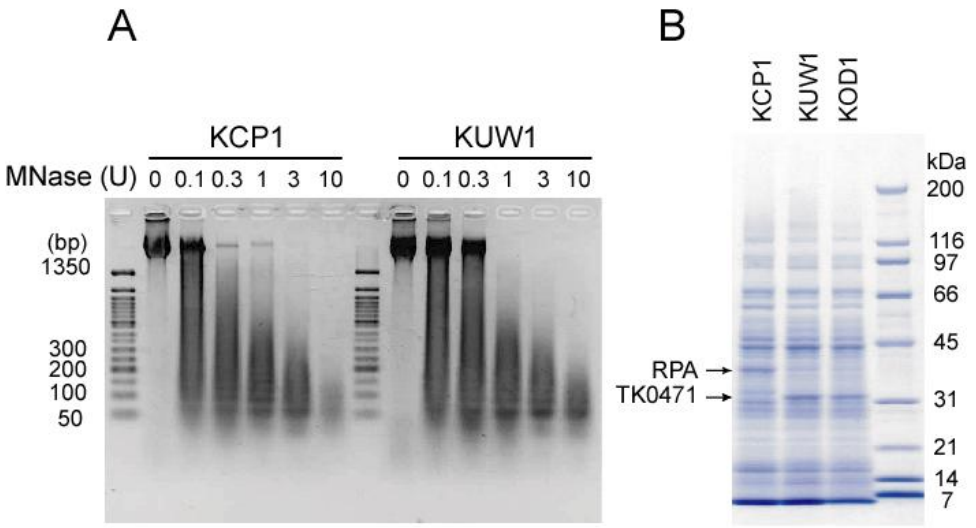

Figure 12

Figure 12. Analysis of the ΔTK0471 strain

(A) Sensitivity of the chromatin fractions of (left) KCP1 and (right) KUW1 to MNase digestion. Chromatin fractions were incubated with increasing amounts of MNase (0, 0.1, 0.3, 1, and 10 U) at 37°C for 1 h. DNA was purified and separated on 2.5% agarose in 0.5x TBE buffer. (B) Proteins in the chromatin fractions of the KOD1, KUW1, and KCP1 strains were compared by means of SDS-PAGE on a 5–20% gradient gel. In the KCP1 strain, the ~32-kDa protein band disappeared and a band of ~35 kDa appeared. The ~35-kDa band was identified through mass spectrometry as consisting of RPAs. See also Figure 10.

The chromatin fraction of the KCP1 strain was more sensitive to MNase digestion than that of the wild-type KUW1 strain was (Figure 12A). Digestion with 0.3 units of MNase resulted in an almost complete removal of high molecular weight genomic DNA from the chromatin fraction of KCP1, whereas high molecular weight genomic DNA was left partially undigested in the chromatin fraction of KUW1 (Figure 12A). MNase digestion of the chromatin fraction of the KCP1 cells still resulted in the laddered pattern of DNA in the low molecular weight region that is characteristic of nucleosome formation (Figure 12A).

A protein band with an apparent molecular mass of ~35 kDa accumulated in the chromatin fraction of the KCP1 strain, though there was no obvious change in the patterns of other proteins compared to their patterns in the wild type strains (KOD1 and KUW1) (Figure 12B). Mass spectrometric analysis revealed that the ~35-kDa band contained TK1959 and TK1961 proteins, which are archaeal homologues of eukaryotic replication protein A (RPA) complex subunits (Komori and Ishino, 2001).

3-6 TK0471 deletion results in up-regulation of specific genes in log phase

cDNAs generated from the RNA preparations of the wild type (KUW1) and ΔTK0471 (KCP1) cells grown to the log phase in ASW-YT-S^0 medium were labeled with Cy3 and Cy5, respectively, and hybridized to the *T. kodakarensis* genomic array, which has spots that represent all 2306 predicted ORFs identified in the *T. kodakarensis* genome (Fukui *et al.*, 2005). The entire result is shown in Appendix C, and summarized in Figure 13. In the KCP1 strain, the signal intensities of 151 ORFs on the genome (6.5% of the total) were elevated more than twofold compared to those in the wild-type KUW1 strain. However, 41 ORFs (1.8% of the total) were decreased more than twofold. The number of ORFs that did not exhibit a significant (i.e. twofold or greater) alteration was 1974.

The alteration in transcript level had a strong correlation with the presence of TK0471 protein on the promoter region in the log phase, which was determined by the sequencing of DNA in the heavy fraction (Figure 9 and Appendix B). The signal intensity ratio (Log_2[KCP1/KUW1]) of the ORFs that exhibited TK0471 enrichment in the promoter region (defined here as -200 to +50 relative to start codon) was 1.76 ± 3.27 (median ± quartile range, n = 90, Figure 14A and Table 2). This was significantly higher than that of the ORFs with TK0471 enrichment in the coding region (-0.12 ± 0.59, n = 293, Figure 14B), or that of the ORFs that did not have significant enrichment of TK0471 (–0.16 ± 0.56, n = 1776, Figure 14C) (P < 6.6e -16 in both cases, Wilcoxon rank sum test with Bonferroni correction). Signal intensity ratios of individual ORFs, together with the list of TK0471 enrichment, can be found in Appendix C.

Transcript levels of ORFs in the KCP1 strain in the stationary phase were also determined (Appendix C). Results were obtained for 1253 out of 2306 ORFs. The signals of the other ORFs could not be detected, probably due to degradation of the RNA in the stationary phase. Among the 1253 ORFs for which transcript levels were determined, 192 exhibited elevated (greater than twofold) signal intensities compared to those in the wild-type KUW1 strain, while 224 exhibited decreased (greater than twofold) signal intensities. The number of ORFs that did not exhibit significant (i.e. twofold or greater) difference between KCP1 and KUW1 was 837.

In contrast to the log phase, TK0471 enrichment to the promoter did not correlate with alteration of the transcript level in the ΔTK0471 strain (KCP1) in the stationary phase. The signal intensity ratio (Log_2[KCP1/KUW1]) of the ORFs that exhibited TK0471 enrichment in the promoter region (-200 to +50 relative to start codon) was 0.38 ± 0.84 (median ± quartile range, n = 11), which is not significantly different from that of the ORFs with TK0471 enrichment in the coding region (-0.41 ± 1.07; n = 57), or from that of the ORFs without any TK0471 enrichment (–0.16 ± 1.34; n = 1185) (P = 0.53 and P = 0.11, respectively). The complete set of microarray results, together with the list of ORFs with TK0471 enrichment, is shown in Appendix C.

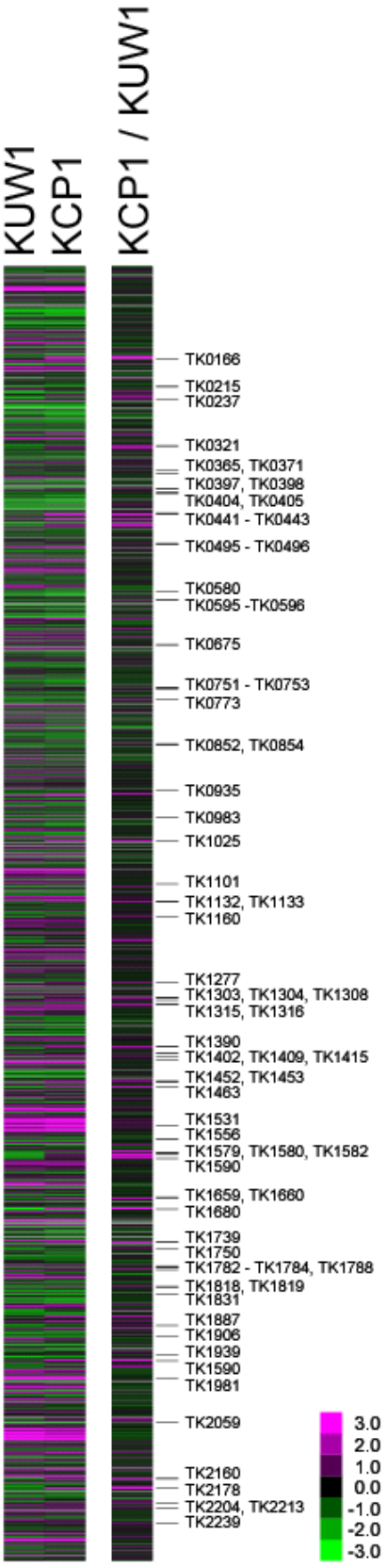
KUW1
KCP1
KCP1 / KUW1
TK0166
TK0215
TK0237
TK0321
TK0365, TK0371
TK0397, TK0398
TK0404, TK0405
TK0441 - TK0443
TK0495 - TK0496
TK0580
TK0595 -TK0596
TK0675
TK0751 - TK0753
TK0773
TK0852, TK0854
TK0935
TK0983
TK1025
TK1101
TK1132, TK1133
TK1160
TK1277
TK1303, TK1304, TK1308
TK1315, TK1316
TK1390
TK1402, TK1409, TK1415
TK1452, TK1453
TK1463
TK1531
TK1556
TK1579, TK1580, TK1582
TK1590
TK1659, TK1660
TK1680
TK1739
TK1750
TK1782 - TK1784, TK1788
TK1818, TK1819
TK1831
TK1887
TK1906
TK1939
TK1590
TK1981
TK2059
TK2160
TK2178
TK2204, TK2213
TK2239
3.0
2.0
1.0
0.0
-1.0
-2.0
-3.0

Figure 13

Figure 13. Transcriptome analysis in *T. kodakarensis* KUW1 and KCP1 strains in the log phase

Transcript levels of each predicted ORF in KUW1 and KCP1, as well as the "KCP1/KUW1" ratio, are indicated by color. Magenta represents relatively high signal intensity while green indicates relatively low signal intensity. In the right column, magenta indicates a high signal intensity ratio, while green indicates a low signal intensity ratio (Log_2[KCP1/KUW1]). ORFs with no data are indicated in gray. ORFs that exhibited TK0471 enrichment in the promoter region are indicated on the right.

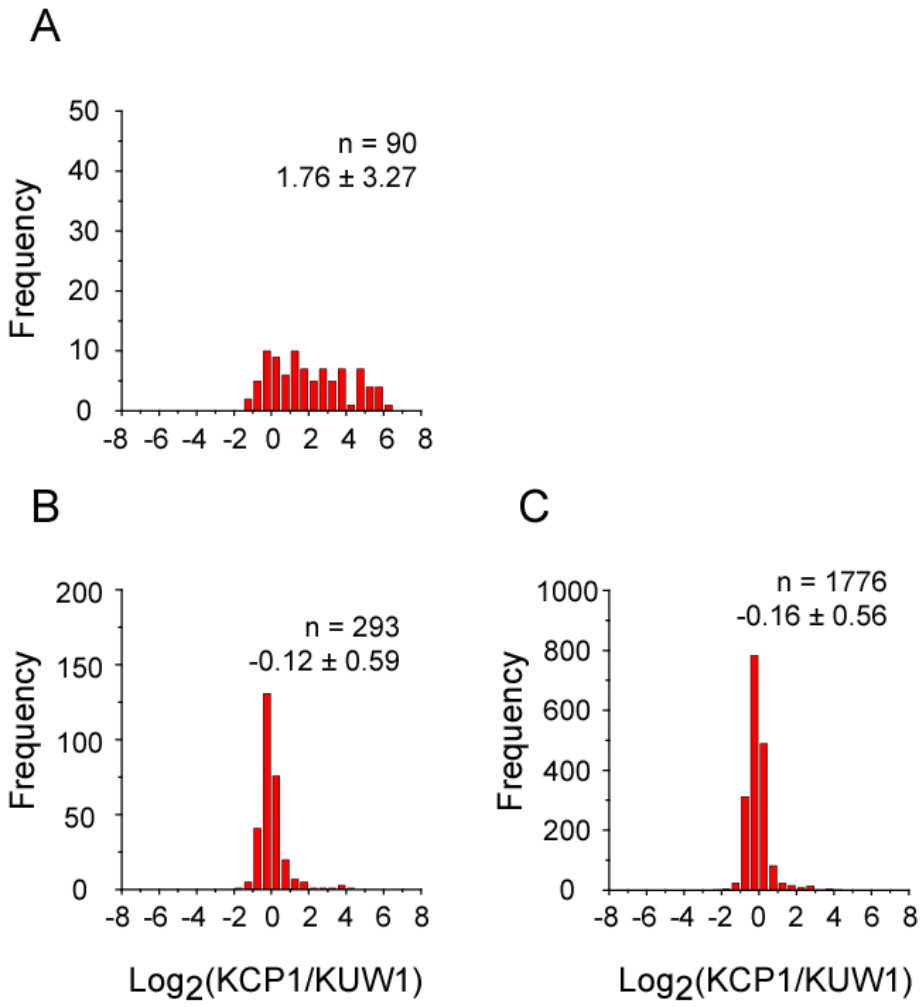

Figure 14

Figure 14 Signal intensity ratios (Log_2[KCP1/KUW1]) of ORFs

Classified according to whether TK0471 is (A) bound to a promoter region (-200 to +50 relative to start codon), (B) bound to a coding region, or (C) not bound to any region, are indicated by histograms. The median ± quartile range of each sample is indicated. Promoter binding of TK0471 correlates with transcript elevation in the ΔTK0471 strain (KCP1). See also Table 2 and Appendix C.

Table 2: ORFs with TK0471 localization on the promoter region (-200 to +50 relative to start codon) in log phase, together with their transcript alteration in Δ TK0471strain (KCP1) in log phase. Boxes indicate ORFs in the same (predicted) operon.

Gene ID	Annotation	TK0471 position	Intencity ratio Log_2(KCP1/KUW1)	
			Mean	SD
TK0161	ABC-type multidrug transport system, ATPase component_COG1131	operon	2.30	0.27
TK0162	Hypothetical membrane protein	operon	3.21	0.01
TK0163	Hypothetical membrane protein, conserved	operon	3.63	0.11
TK0164	S-layer-like array protein	operon	3.95	0.05
TK0165	Hypothetical protein	operon	4.58	0.17
TK0166	Hypothetical protein	-28	4.83	0.03
TK0215	Hypothetical protein, conserved	-59	0.29	0.18
TK0237	Hypothetical membrane protein	+34	1.03	0.34
TK0321	Hypothetical protein	+8	3.88	0.18
TK0365	Membrane-bound phosphoesterase, PAP2 superfamily	-91	1.25	0.03
TK0371	Hypothetical protein	+50	-0.44	0.42
TK0397	Hypothetical membrane protein, conserved	-72	0.89	0.10
TK0398	Hypothetical protein	-15	1.20	0.11
TK0404	Hypothetical protein, conserved	-91	0.38	0.08
TK0405	Predicted transcription regulator, SpoVT/AbrB family_COG2002	-132	-0.14	0.06
TK0406	Predicted transcription regulator, SpoVT/AbrB family_COG2002	operon	-0.78	0.33
TK0441	FKBP-type peptidyl-prolyl cis-trans isomerase, fused to C-terminal uncharacterized domain_COG	-115	0.15	0.02
TK0442	Hypothetical protein, conserved	-54	5.71	0.35
TK0443	Hypothetical membrane protein	operon	4.57	0.36
TK0495	Probable transposase_COG0675	-35	1.82	0.03
TK0496	Hypothetical membrane protein	-83	0.16	0.68
TK0580	Hypothetical protein	+19	-0.55	0.06
TK0595	Hypothetical membrane protein	-138	-1.16	0.17
TK0596	Hypothetical membrane protein	-30	2.04	0.10
TK0675	Hypothetical protein, conserved, radical SAM superfamily_COG0641	-171	0.37	0.03
TK0751	Hypothetical protein, conserved	-30	1.25	0.21
TK0752	Acylamino acid-releasing enzyme (acylaminoacyl-peptidase)_COG1506	-138	-0.72	0.24
TK0753	Hypothetical membrane protein	-72	1.05	0.14
TK0773	Predicted ATP-dependent endonuclease, OLD family_COG3593	-51	2.64	0.09
TK0852	Hypothetical protein, conserved, radical SAM superfamily	+46	0.35	0.07
TK0854	Cobyric acid synthase_COG1492	+7	-0.05	0.33
TK0935	TRAP-type transporter, periplasmic component_COG2358	+32	-0.11	0.18
TK0983	Hypothetical protein	+4	0.10	0.09
TK1024	Hypothetical membrane protein	operon	4.99	0.33
TK1025	Hypothetical protein, conserved, containing ATP/GTP-binding site motif A	-163	4.73	0.21
TK1101	RNA-binding protein, Nop10p family_COG2260	+41	-0.39	0.19
TK1132	Hypothetical membrane protein	-43	1.89	0.03
TK1133	Hypothetical protein	+43	2.10	0.10
TK1160	Hypothetical membrane protein	-2	1.27	0.18
TK1277	Hypothetical membrane protein	+15	3.70	0.45
TK1303	Hypothetical protein, conserved	-55	2.23	0.18
TK1304	Hypothetical protein, conserved	-85	2.52	0.16
TK1308	Hypothetical protein	-38	2.01	0.02
TK1315	3'-Phosphoadenosine 5'-phosphosulfate reductase, fused to RNA-binding PUA and 4Fe-4S bindir	-104	-0.26	0.10
TK1316	Predicted membrane protease subunit, stomatin/prohibitin homolog_COG0330	-14	3.42	0.07
TK1390	Hypothetical protein, conserved	+6	5.49	0.32
TK1402	Polysaccharide deacetylase_COG3233	-51	1.71	0.16
TK1409	Hypothetical membrane protein	+30	1.56	0.18
TK1415	LSU ribosomal protein L12A_COG2058	+31	0.55	0.09
TK1452	ABC-type multidrug transport system, ATPase and permease components_COG1132	-103	2.80	0.12
TK1453	Hypothetical protein, conserved	-98	3.45	0.44
TK1463	Hypothetical protein, conserved	-98	6.33	0.06
TK1531	LSU ribosomal protein L14P_COG0093	+20	0.71	0.19
TK1556	ATPase, PP-loop superfamily_COG0037	+7	-0.15	0.14
TK1577	Hypothetical membrane protein, conserved_COG1470	operon	2.54	0.06
TK1578	Hypothetical membrane protein, conserved_COG1277	operon	3.71	0.42
TK1579	ABC-type multidrug transport system, ATPase component_COG1131	-30	ND	ND
TK1580	Hypothetical protein, conserved, UPF0153 family_COG0727	-108	0.48	0.39
TK1582	Hypothetical membrane protein	-92	5.81	0.16
TK1583	Hypothetical protein	operon	2.69	0.20
TK1584	Hypothetical membrane protein	operon	2.62	0.11
TK1585	Hypothetical protein	operon	2.55	0.09
TK1590	Predicted ATPase, AAA superfamily_COG0467	-2	1.48	0.02
TK1591	Predicted transcription regulator, encoded next to RecA superfamily ATPase_COG1318	operon	1.33	0.33

Table 2 continued

TK1659	Small neutral amino acid transporter_COG2095	-27	-0.06	0.09
TK1660	Hypothetical protein, conserved	-87	5.12	0.39
TK1680	Hypothetical protein	-32	5.53	0.18
TK1739	Hypothetical protein	-32	3.29	0.12
TK1740	Hypothetical membrane protein, conserved	operon	1.86	0.36
TK1750	Hypothetical protein, conserved	+14	3.62	0.34
TK1782	Serine protease inhibitor Serpin homolog_COG4826	+22	0.68	0.04
TK1783	Hypothetical membrane protein	-83	1.07	0.00
TK1784	Predicted SAM-dependent methyltransferase, DUF890 family_COG0500	-110	-0.15	0.06
TK1787	Hypothetical membrane protein, conserved, DUF112 family_COG1784	operon	1.50	0.00
TK1788	Hypothetical protein, conserved	-107	1.85	0.23
TK1818	Hypothetical protein, conserved	-26	5.39	0.26
TK1819	Capsular polysaccharide biosynthesis protein_COG2244	-162	-0.10	0.15
TK1829	Permease, major facilitator superfamily_COG0477	operon	-0.72	0.08
TK1830	Probable alpha-amylase, GH57 family_COG1543	operon	-	-
TK1831	Galactokinase_COG0153	-124	-0.78	0.02
TK1887	Hypothetical membrane protein	+47	1.09	0.08
TK1906	Hypothetical protein	-166	0.11	0.04
TK1939	Hypothetical protein, conserved	+47	0.96	0.27
TK1950	Hypothetical protein	-117	5.07	0.05
TK1981	2-Oxoisovalerate:ferredoxin oxidoreductase, beta subunit_COG1013	+18	-1.07	0.23
TK2059	Hypothetical protein	-44	-	-
TK2160	Hypothetical protein, conserved, radical SAM superfamily_COG0641	-117	4.67	0.16
TK2161	ABC-type multidrug transport system, ATPase component_COG1131	operon	4.50	0.20
TK2162	Hypothetical membrane protein, conserved	operon	3.80	0.23
TK2178	Hypothetical protein, containing ATP/GTP-binding site motif A	+23	4.12	0.22
TK2204	Hypothetical protein, conserved	-103	3.42	0.32
TK2213	Bipolar DNA helicase_COG0433	+40	0.61	0.10
TK2239	PhoI-related type II restriction endonuclease	+12	5.50	0.46

Table 2. List of ORFs with TK0471 localization within the promoter region

Signal intensity ratio (Log_2[KCP1/KUW1]) of the ORFs that exhibited TK0471 localization in the promoter region in log phase. TK0471 position was defined as the middle nucleotide position of the genomic region highly concentrated (more than twofold) in the TK0471-rich heavy fraction (#8) in the log phase. “operon” indicates ORFs in an operon with TK0471 binding to the promoter of the first gene. The mean intensity ratio (KCP1/KUW1) is expressed as a log_2 value with standard deviation (SD). ND indicates a lack of intensity ratio as a result of low signals.

4. Discussion

The present study had four major findings: (i) In addition to histone, a considerable amount of TK0471 protein exists on the chromosome of the hyperthermophilic archaeon *T. kodakarensis*. (ii) TK0471 forms a thick fibrous structure distinct from the archaeal nucleosome array, providing heterogeneity in chromosome architecture. (iii) TK0471 acts as an architectural protein for chromosomes as well as a global transcriptional repressor. (iv) The localization of TK0471 changes dynamically depending on the growth stage of the cells.

4-1 Archaeal genome architecture

The results of the reconstitution experiment (Figure 8) suggest that, among the major DNA-binding proteins on the *T. kodakarensis* chromosome, histone is the only one that contributes to compaction by wrapping genomic DNA. Digestion of the isolated chromatin fraction with MNase resulted in a characteristic laddered pattern of DNA (~60, ~90, 120, 150 bp etc., Figure 5C). The ~60- and ~90-bp DNA fragments correspond to the length of the fragment that makes direct contact with the histone-fold of the archaeal histone tetramer, and to the length of the fragment that fully circumvents the histone core, respectively (Pereira *et al.*, 1997; Pereira and Reeve, 1999). ~120 bp of DNA correspond to the length of DNA that is wrapped around a histone tetramer (Tomschik *et al.*, 2001). The longer DNA fragments (~150 bp and larger) may correspond to the lengths of fragments that are in contact with more than one histone tetramer.

In the *T. kodakarensis* genome, the TK0471 protein forms a thick fibrous structure (Figure 7B and 8F). Even in the histone-encoding euryarchaeal species, histone-based DNA wrapping is not the only mechanism that plays a role in genome organization. Indeed, earlier electron microscopic studies of the chromosome of the halophilic euryarchaeon *Halobacterium salinarium* have shown that nucleosome-free regions exist on the chromosome (Shioda *et al.*, 1989; Takayanagi *et al.*, 1992). On the basis of its distribution throughout the chromosome, I propose that TK0471/TrmBL2 is a novel chromosomal protein that all species in the order Thermococcales possess (see below). In support of this notion, TrmBL2 of *Pyrococcus furiosus* (PF0496) was shown to be one of the proteins in the cell extract that can bind to DNA in a sequence-independent manner *in vitro* (Lipscomb *et al.*, 2009). Besides, a whole-genome proteomics study has shown that *Thermococcus gammatolerans* TrmBL2 (TGAM_1678 or tg1678) is much more abundant in the cell than other normal transcription factors (Zivanovic *et al.*, 2009).

I show here that the protein Alba of *T. kodakarensis* can form, *in vitro*, a short fibrous structure on dsDNA (Figure 8G). This structure is similar in diameter to that of the "helical protein fiber" formed in the presence of the Alba of the Sulfolobus species, as observed by electron microscopy (Lurz *et al.*, 1986) or modeled from the crystal structure (Wardleworth *et al.*, 2002). However, such a structure was not identified in the light fractions of the chromatin isolated from the cell (Figure 7A). This is likely due to the small amount of Alba relative to histone. Because the distribution of Alba overlaps with and cannot completely be separated from that of histone in the experimental system, I did not determine the localization of Alba along the genome. A chromatin immunoprecipitation approach would be necessary in the future to identify the precise localization of Alba. It has also been shown that Alba can hold two DNA duplex together *in vitro* (Lurz *et al.*, 1986; Jelinska *et al.*, 2005). Although I could not detect such a structure under the condition that I have used (for instance, I used a linear instead of circular DNA molecule), it might occur *in vivo*.

The *T. kodakarensis* chromosome undergoes dynamic structural changes during the transition from the log phase to the stationary phase (Figure 3). Since chromosome condensation still occurs in the ΔTK0471 strain (KCP1) (Figure 11B), TK0471 is not essential for chromosome condensation. The slight difference in the protein composition of the chromatin fraction between the log and stationary phases (Figure 5B) might be involved in the chromosome condensation in the stationary phase. It would be interesting to figure out in the future which of these proteins are responsible for the chromosome condensation in the stationary phase.

4-2 Physiological roles of TK0471/TrmBL2

Sequencing of DNA co-enriched with TK0471 illustrates that this protein localizes both to the coding regions and to the intergenic regions *in vivo* (Figure 9). This mode of localization is similar to that of the bacterial nucleoid-associated proteins, such as IHF and H-NS (Grainger *et al.*, 2006) and several recently studied archaeal transcription factors and regulators (Koide *et al.*, 2009). A significant correlation between TK0471's binding to the promoter region and alteration of the transcript levels of downstream genes (Figure 14A) suggests that TK0471 directly binds to some promoter regions and represses their transcription, probably by blocking RNAP's access. The thick fibrous structure would, in this case, be formed by the binding of TK0471 to dsDNA, followed by the incorporation of more proteins into the adjacent region of the DNA through protein-protein interactions in a manner similar to that by which H-NS binds to DNA (Bouffartigues *et al.*, 2007; Lang *et al.*, 2007). A significant number of the ORFs that

were identified as being under direct control of TK0471 are classified as hypothetical proteins by genome annotation (Fukui *et al.*, 2005). The exact cellular role of these proteins in archaeal life is not known; additional experiments will be required for their characterization.

In contrast to TK0471's binding to promoters, which represses transcription, TK0471's binding to coding regions does not disrupt transcription elongation (Figure 14B). Since the microarray used in this study contains ~300 bp of DNA corresponding to the 3' region of each predicted ORF, I was able to determine that RNAP transcribes throughout the entire coding sequence, rather than halting in the middle. TK0471's binding to the coding region may play as-yet-unidentified roles in genome structure and function. My results suggest that one of these roles could consist of shaping the genetic material into a structure that makes it less accessible to enzymes or other proteins (Figure 12A).

It is interesting to note that, although the transcript levels of more than 150 ORFs vary by more than twofold between the wild type (KUW1) and the ΔTK0471 strain (KCP1), only RPA proteins highly accumulated in the chromatin (Figure 12B). The transcripts of RPA subunit genes (TK1959 and TK1961) were approximately 4 to 6 times more abundant in the ΔTK0471 strain (2.53 ± 0.21 and 2.16 ± 0.10 respectively in Log_2 scale), which rank 60th ~ 80th on the list of ORFs with high ΔTK0471/wild-type transcript ratio (Appendix C). The high transcript level of the RPA genes, together with its reported DNA-binding activity (Komori and Ishino, 2001), may explain the abundance of RPA protein in the chromatin of the ΔTK0471 strain. The questions of whether the RPA transcription is under direct control of TK0471, and what physiological significance it has, are unresolved at present.

Given that TK0471 localizes to specific promoter regions of the chromosome, the existence of a consensus recognition sequence was expected, but an extensive search consisting of sequence analysis of DNA concentrated with TK0471 has thus far identified no candidates for such a consensus recognition sequence. I also did not detect any significant difference in the bending propensity of the DNA sequence compared to the whole genome, using the trinucleotide flexibility parameter described previously (Brukner *et al.*, 1995; Fukue *et al.*, 2004). It can be speculated that TK0471 might localize specifically to relatively nucleosome-free regions without having its own specific recognition sequence. It has been shown that archaeal histone, like eukaryotic histone, prefers certain sequence motifs (nucleosome positioning signals) when binding to DNA (Bailey *et al.*, 2000).

4-3 TK0471/TrmBL2 forms a superfamily

TK0471 shares amino acid sequences homologous to the transcription factors TrmB (transcriptional regulator of mal operon) and Tgr/TrmBL1 (Thermococcales glycolytic regulator / TrmB-like 1) of Thermococcales, and thus was previously named TrmBL2 (TrmB-like 2) (Kanai *et al.*, 2007; Lee *et al.*, 2007; Lee *et al.*, 2008). A search of the Pfam database (Pfam 24.0, October 2009, http://pfam.sanger.ac.uk/) revealed that these proteins each consist of two domains, TrmB (Pfam ID: PF01978) and Regulator_TrmB (Pfam ID: PF11495). The TrmB domain is a member of the helix-turn-helix (HTH) DNA-binding domain, and is widely distributed in many bacteria, both gram-positive and gram-negative, as well as in archaea, including most archaeal classes identified so far (Perez-Rueda and Janga, 2010) (Appendix D). The TrmB domain is found in 40 archaeal and 99 bacterial genera (out of the total of 48 archaeal and 364 bacterial genera with at least one sequenced genome listed in the KEGG database by April 2010; http://www.kegg.jp/). Among these TrmB domain-containing proteins, there are proteins that consist only of the TrmB domain, as well as proteins that possess domains other than Regulator_TrmB. The variation in domain organization, together with the wide distribution of this domain, suggests that the TrmB domain appeared in the early stage of life history, and that it forms a large superfamily with DNA binding ability.

Proteins with the same domain organization as TK0471/TrmBL2 (i.e. both TrmB and Regulator_TrmB) are found in 18 archaeal and 19 bacterial genera (Figure 15 and 16, Appendix D). Given the total number of genera with sequenced genomes in each domain, namely 48 archaeal and 364 bacterial, this type of protein appears to be more common in archaea than in bacteria. Within the archaea, it is found in 13 genera in Euryarchaeota, 3 genera in Crenarchaeota and 1 genus each in Korarchaeota and Thaumarchaeota. Halobacteriales, Thermococcales and Thermoplasmatales are the euryarchaeal orders that posses this type of protein most frequently (Appendix D). It might have emerged in one of these genera and spread by horizontal gene transfer to other archaeal and bacterial species. It is interesting that this type of protein exists in a limited number of species. Many other chromosomal proteins in prokaryotes are also limited in their gene distribution; for instance, H-NS is conserved only in Gram-negative Gammaproteobacteria, and SarA, which has been proposed as a functional counterpart of H-NS (Fujimoto *et al.*, 2009), is present only in Gram-positive Firmicutes. These facts suggest that prokaryotic species in general have evolved their own chromosomal proteins to organize their chromosomes in conjunction with transcriptional regulation. Further comparative studies between archaea and bacteria would provide more insights into the specific function of this type of proteins.

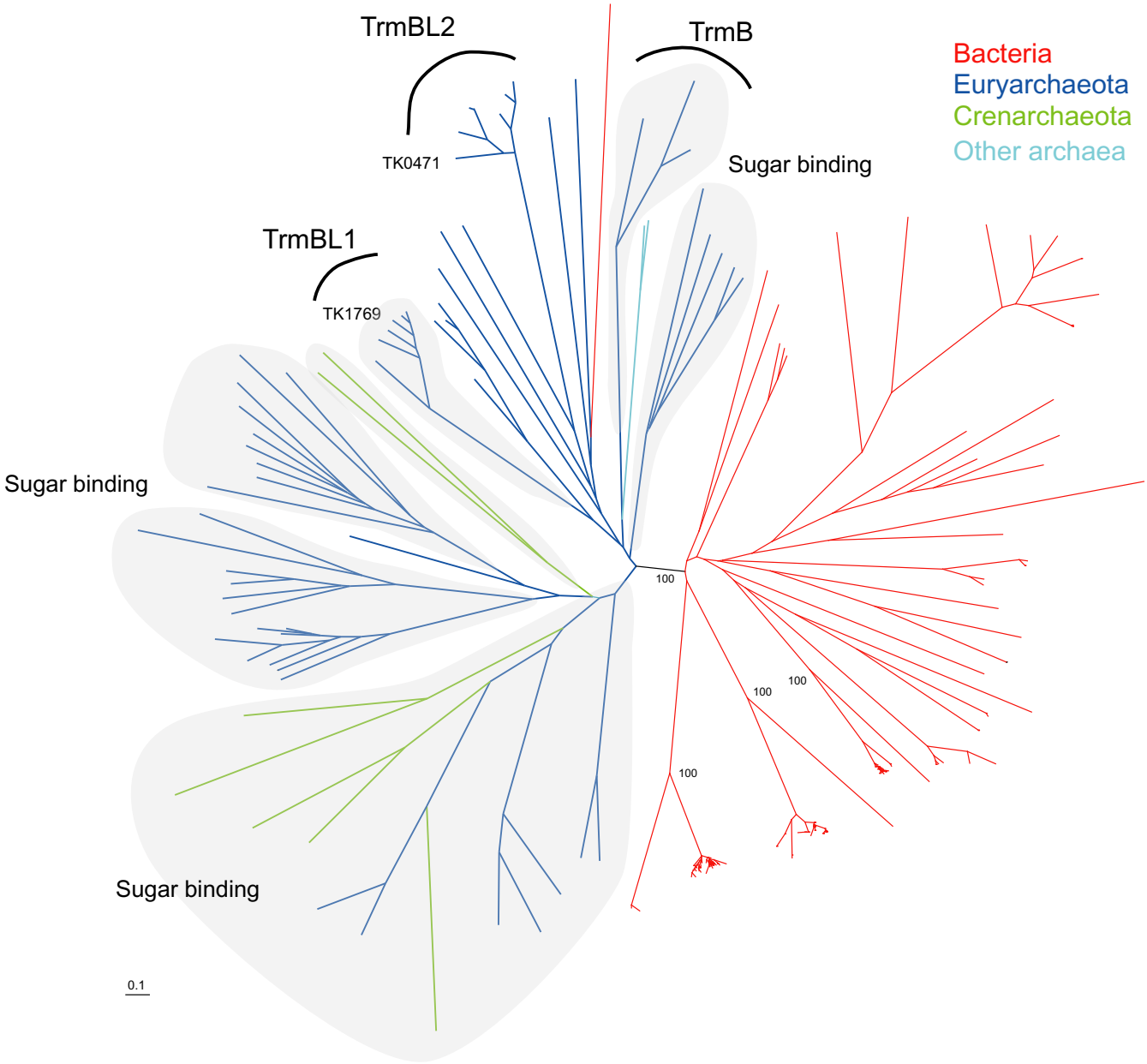

Figure 15

Figure 15. Phylogenetic analysis of proteins that have both TrmB and Regulator_TrmB domains

(A) Unrooted phylogenetic tree of proteins using TrmB and Regulatory_TrmB domains for alignment. Proteins that have a sugar binding domain at the C-terminus of the Regulator_TrmB domain are shaded in gray. For instance, TK0471/TrmBL2 lacks the sugar binding domain. Scale bars indicate the Dayhoff distance among proteins.

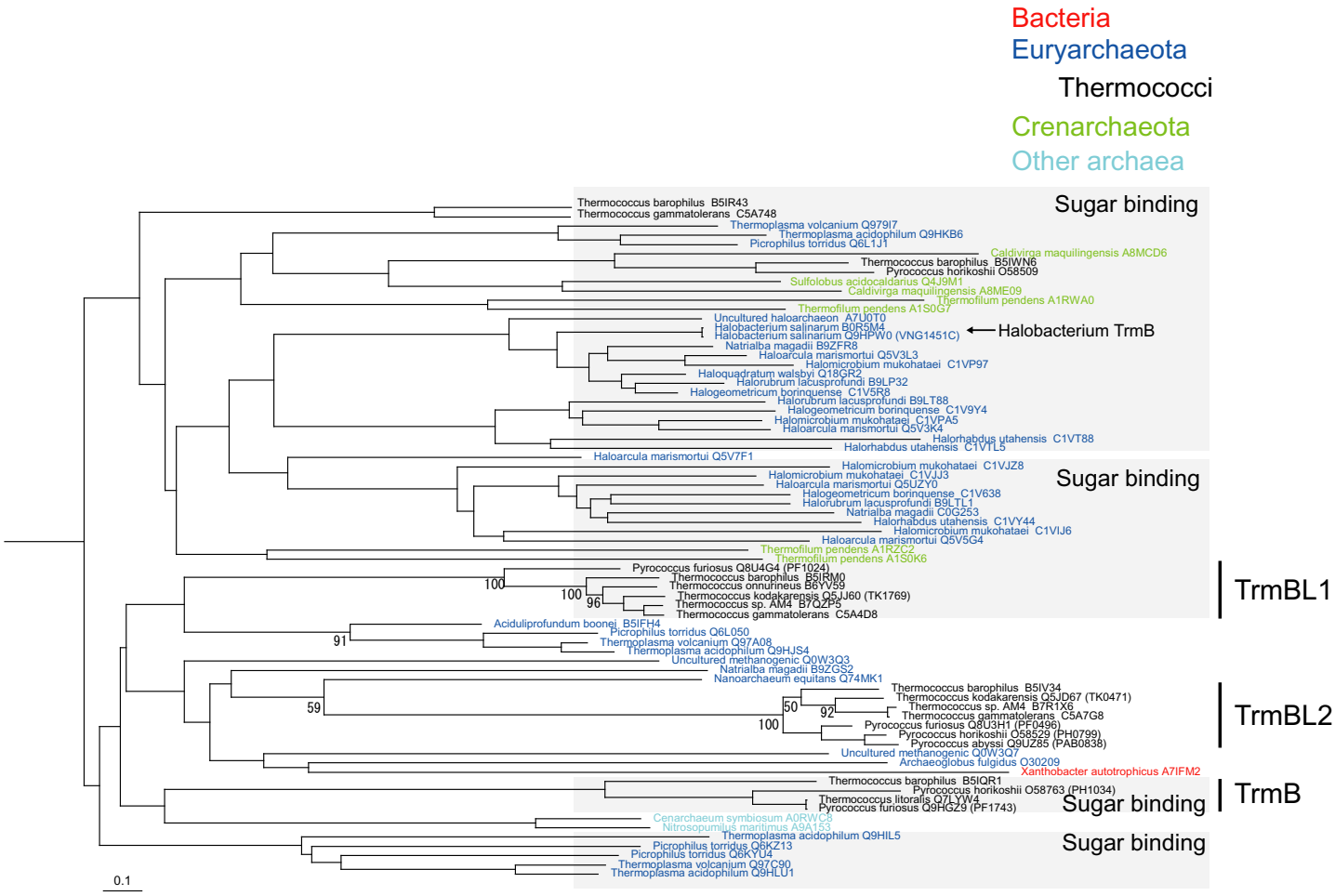

Figure 16

Figure 16 Phylogenetic analysis of proteins that have both TrmB and Regulator_TrmB domains in Archaea.

Magnification of the left half of the tree shown in Figure 15. The UniProt accession number if each protein is indicated. The TrmB family protein of Halobacterium salinarum (VNG1451C) (Schmid et al., 2009) is indicated by an arrow. Proteins that have a sugar binding domain at the C-terminus of the Regulator_TrmB domain are shaded in gray. For instance, TK0471/TrmBL2 lacks the sugar binding domain. Scale bars indicate the Dayhoff distance among proteins.

5. Conclusion and perspective

The existence of a heterogeneous genome architecture in the archaeal chromosome was revealed in this thesis, using a combination of mass spectrometry and atomic force microscopy. During the course of this study, the DNA-binding protein TK0471/TrmBL2 was also discovered as a major chromosomal protein and a global transcription repressor in the hyperthermophilic archaeon *T. kodakarensis*. This protein seems to be a novel type of chromosomal protein common in archaea and bacteria (Maruyama et al., 2011).

The basic building blocks of chromatin (i.e. histone) and the transcription and replication machineries make euryarchaeal chromosome structure similar to eukaryotic chromosome. On the other hand, the newly discovered protein TK0471/TrmBL2 has more similarities to bacterial transcription factors. Its dual roles as a general chromosomal protein and specific transcriptional regulator have a resemblance to the roles of the bacterial nucleoid associated protein H-NS (Rimsky, 2004; Fang and Rimsky, 2008). Therefore, archaeal species seem to have a mixture of bacterial and eukaryotic features; a eukaryote-like nucleosome structure and a bacteria-like gene regulation mechanism.

What biological pathway does the TK0471/TrmBL2 protein control? Although approximately 100 genes were identified as the downstream target of TK0471/TrmBL2, most of these genes were annotated as “hypothetical proteins” (Table 2). Transcriptional regulation by archaeal transcription factors is generally simple. One metabolic pathway is controlled by one transcription factor, which responds to a single environmental factor (Payankaulam *et al.*, 2010). For instance, Tgr/TrmBL1, a paralog of TrmBL2 in Thermococcales, controls glycolitic and gluconeogenic pathways in response to the binding or dissociation of sugar to its C-terminal domain (Kanai *et al.*, 2007; Lee *et al.*, 2007). There is a striking difference between the aforementioned kind of normal transcription factor and the newly discovered TK0471/TrmBL2. TK0471/TrmBL2 does not have the C-terminal ligand-binding domain, and the identified target genes do not belong to an apparent functional category. Further analyses on the effect of TrmBL2 deletion in other species will provide clues as to whether TrmBL2 controls a conserved specific downstream pathway or not.

Another important finding in this thesis was the condensation of the archaeal chromosome in the stationary phase. This suggests the existence of a higher-order folding mechanism in the archaeal chromosome. The dynamic change of chromosome structure seems to be a common phenomenon in all three domains of life. Chromosome

condensation upon stress is common in bacteria and archaea, and cell cycle-dependent chromosome dynamics are common in eukaryotes. The first important step will be to understand the archaeal chromosome condensation mechanism. Since archaea lack the bacterial Dps homolog, one candidate is the archaeal SMC protein. Archaeal SMC proteins are more similar to eukaryotic SMC than bacterial SMC-like proteins (Graumann and Knust, 2009). One can expect that it may play similar roles as eukaryotic SMC does in chromosome dynamics. Understanding the chromosome condensation mechanism in archaeal cells may provide insights into the evolution of eukaryotic chromosome condensation. It would be interesting to further analyze whether the archaeal chromosome structure changes during the cell cycle, and to know if archaeal and eukaryotic chromosome condensation mechanisms are evolutionary related.

In this thesis I analyzed the chromosome structure of only one archaeal species, *T. kodakarensis*. Studies in other types of archaea with different chromosomal proteins will be required to further understand the general genome architecture in archaea, in relation to bacteria and eukaryotes. In this regard, it will be important to study the species in the order Thermoplasmatales, which are euryarchaeotes but encode bacterial HU instead of histone (Table 1). Species in the phylum Crenarchaeaota, which encode Alba but neither histones nor HU (Table 1), will also be important subjects.

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7. Appendices

Appendix A. Whole genome profile of massively parallel DNA sequencing

Appendix B. Genomic regions enriched with histone or TK0471/TrmBL2

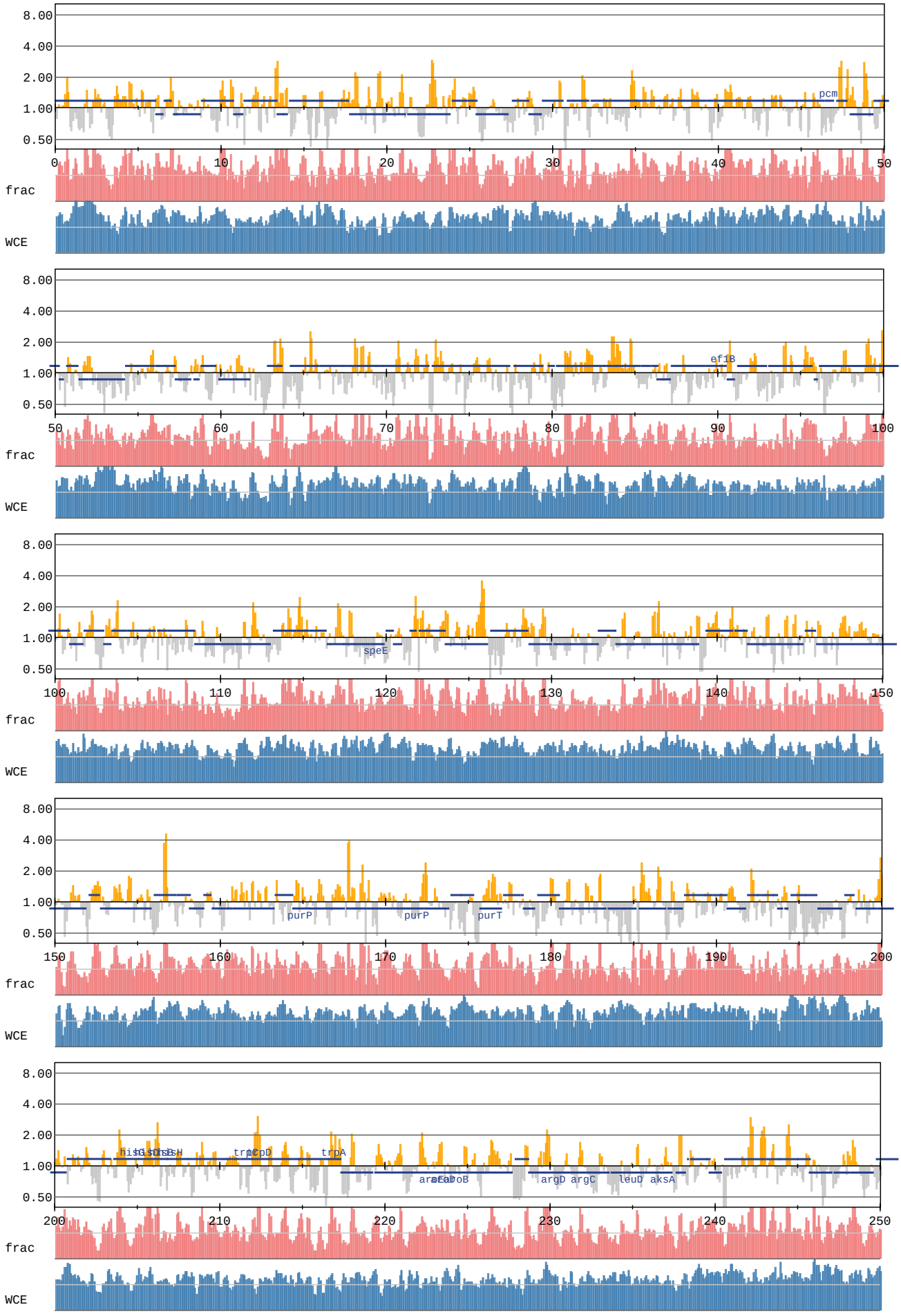
Appendix C. Complete result of microarray analysis

Appendix D. Distribution of TrmB family proteins among the three domains

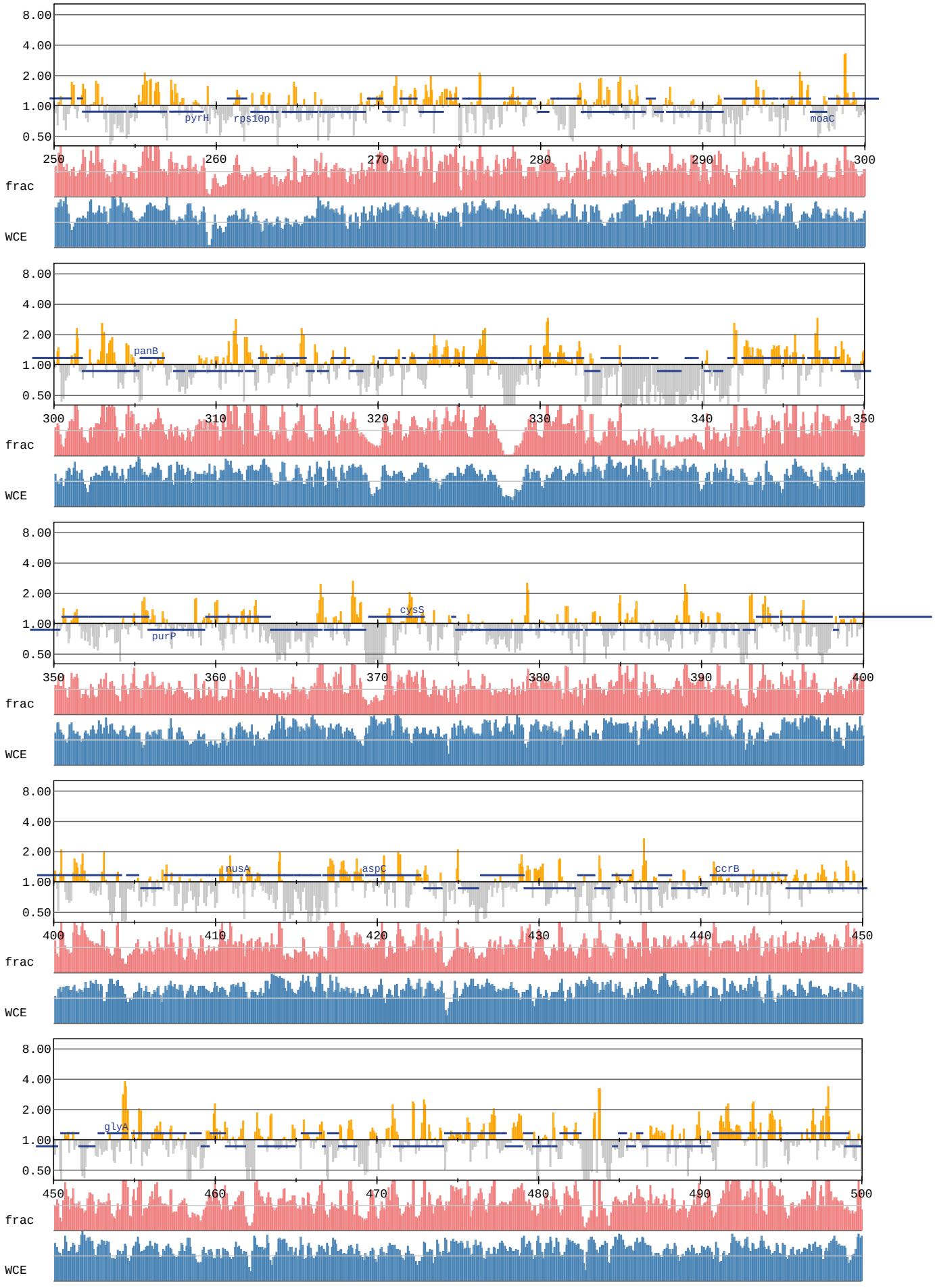
Appendix A. Whole genome profile of massively parallel DNA sequencing

Whole genome profile of massively parallel sequencing of the DNA concentrated in the histone-rich light fraction #3 (pages 1-9) and the TK0471-rich heavy fraction #8 (pages 10-18) of the sucrose density gradient sedimentation of MNase-digested KOD1 chromatin in the log phase, as in Figure 5. “frac” indicates the histogram of DNA sequences concentrated in each fraction. “WCE” indicates the histogram of DNA sequences taken from the whole cell extract.

Histone-rich fraction



Histone-rich fraction



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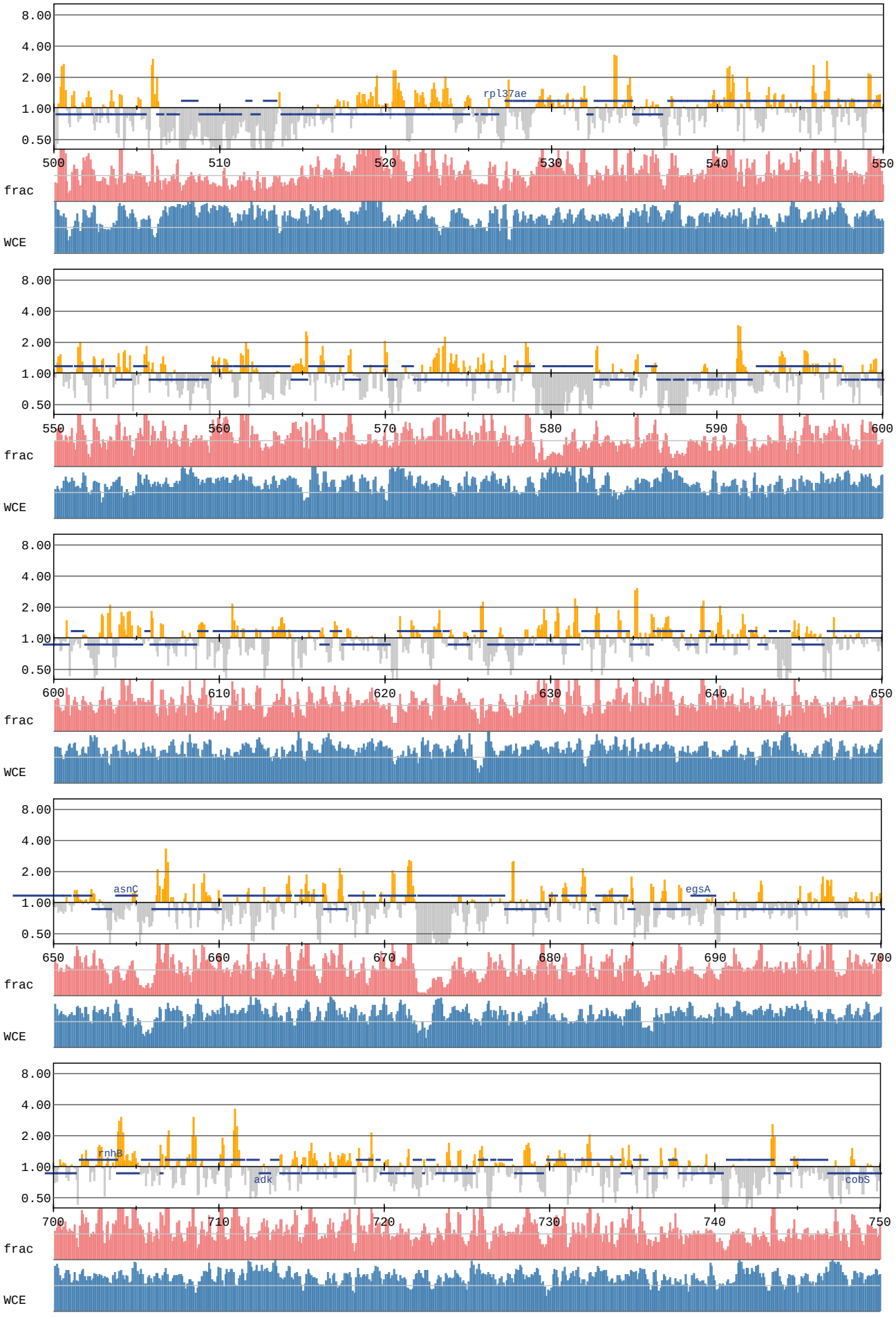

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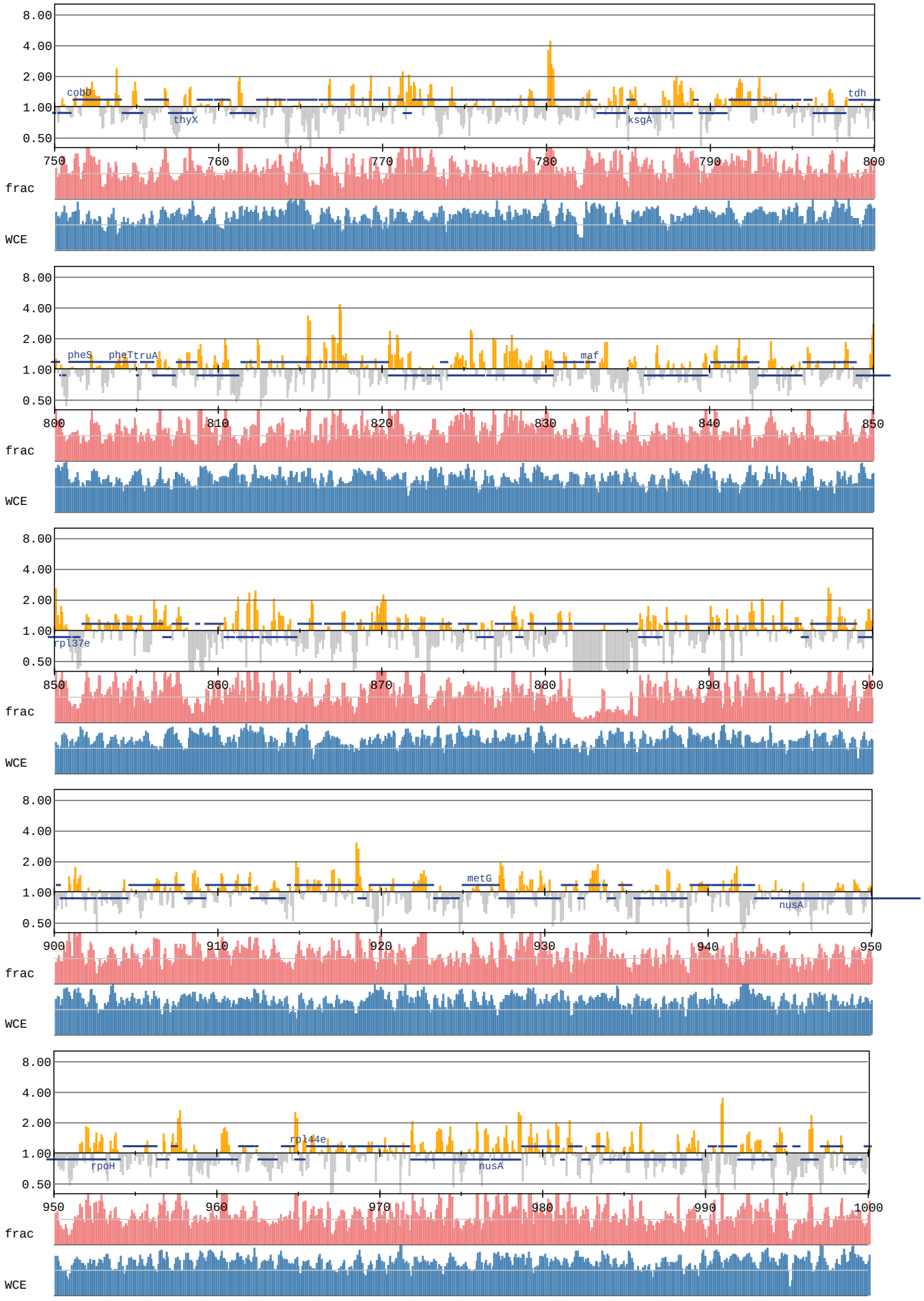

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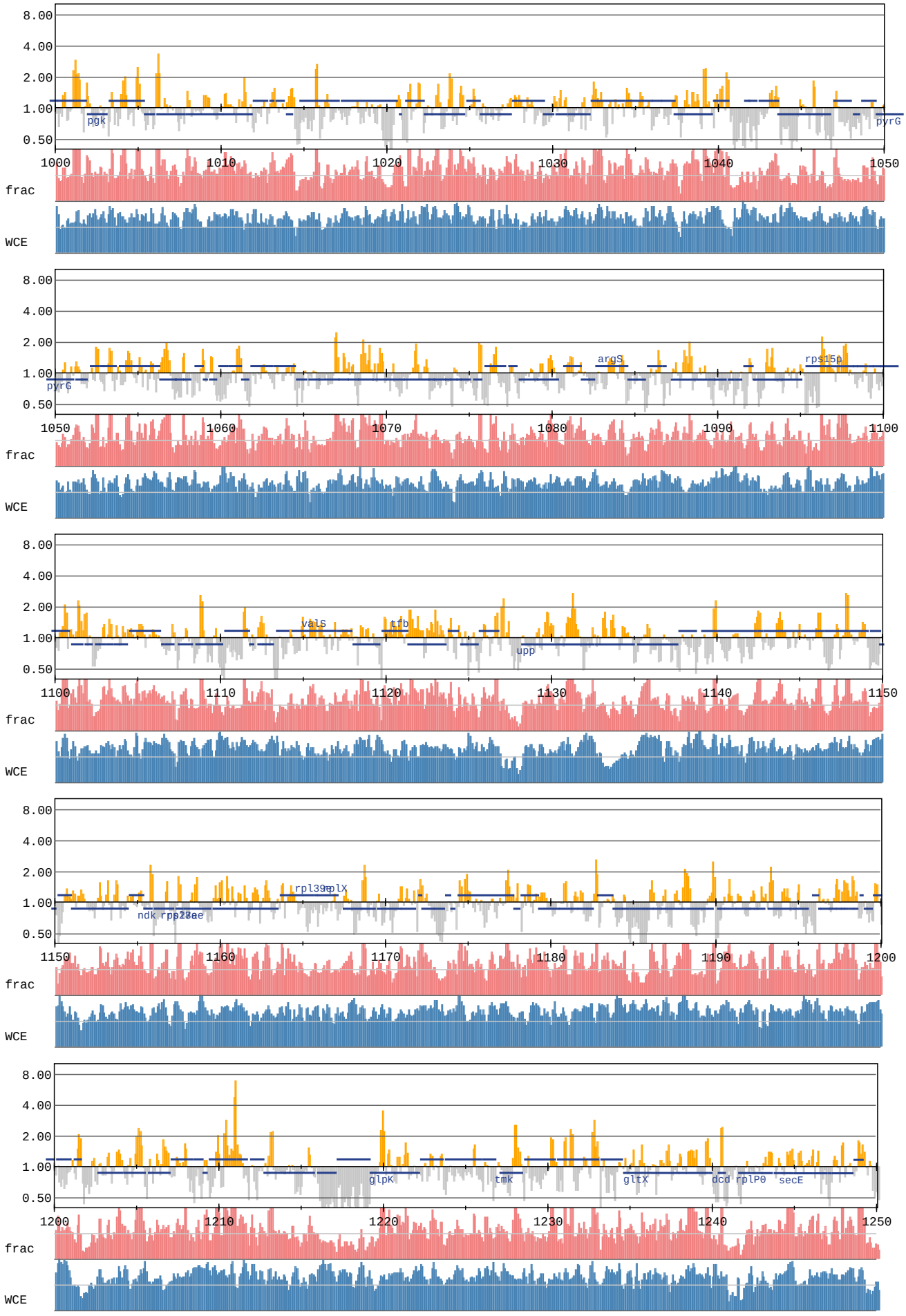

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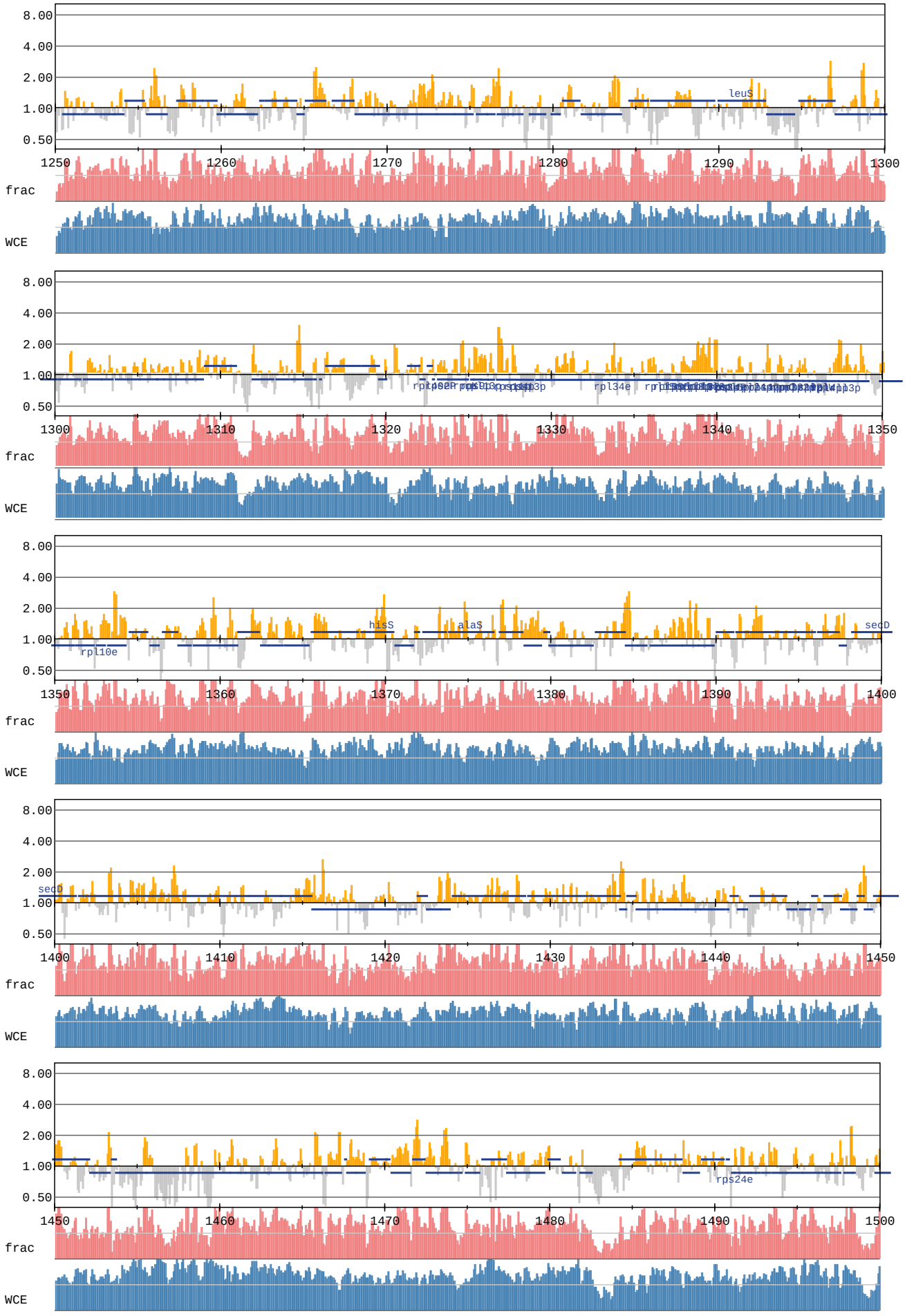

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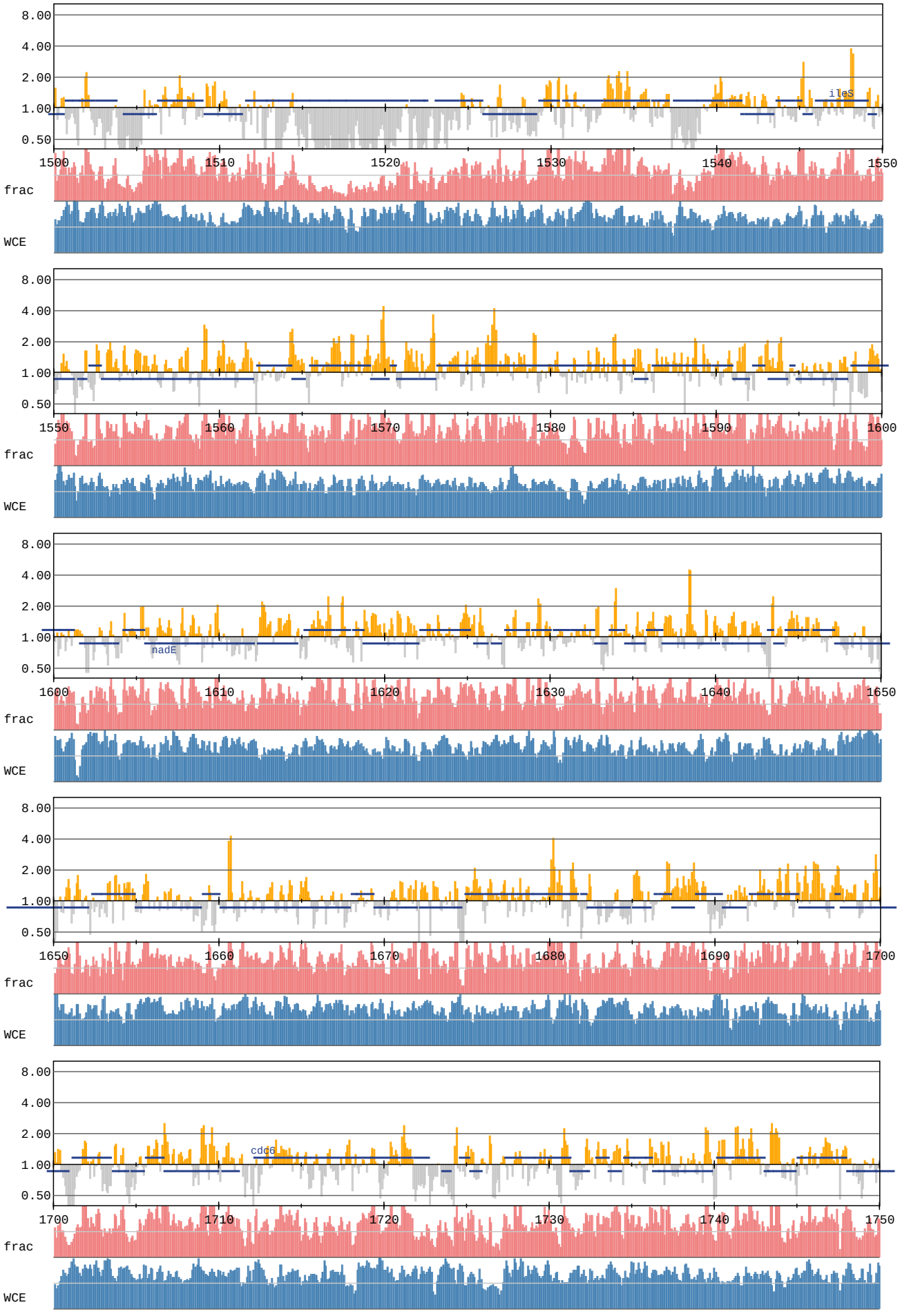

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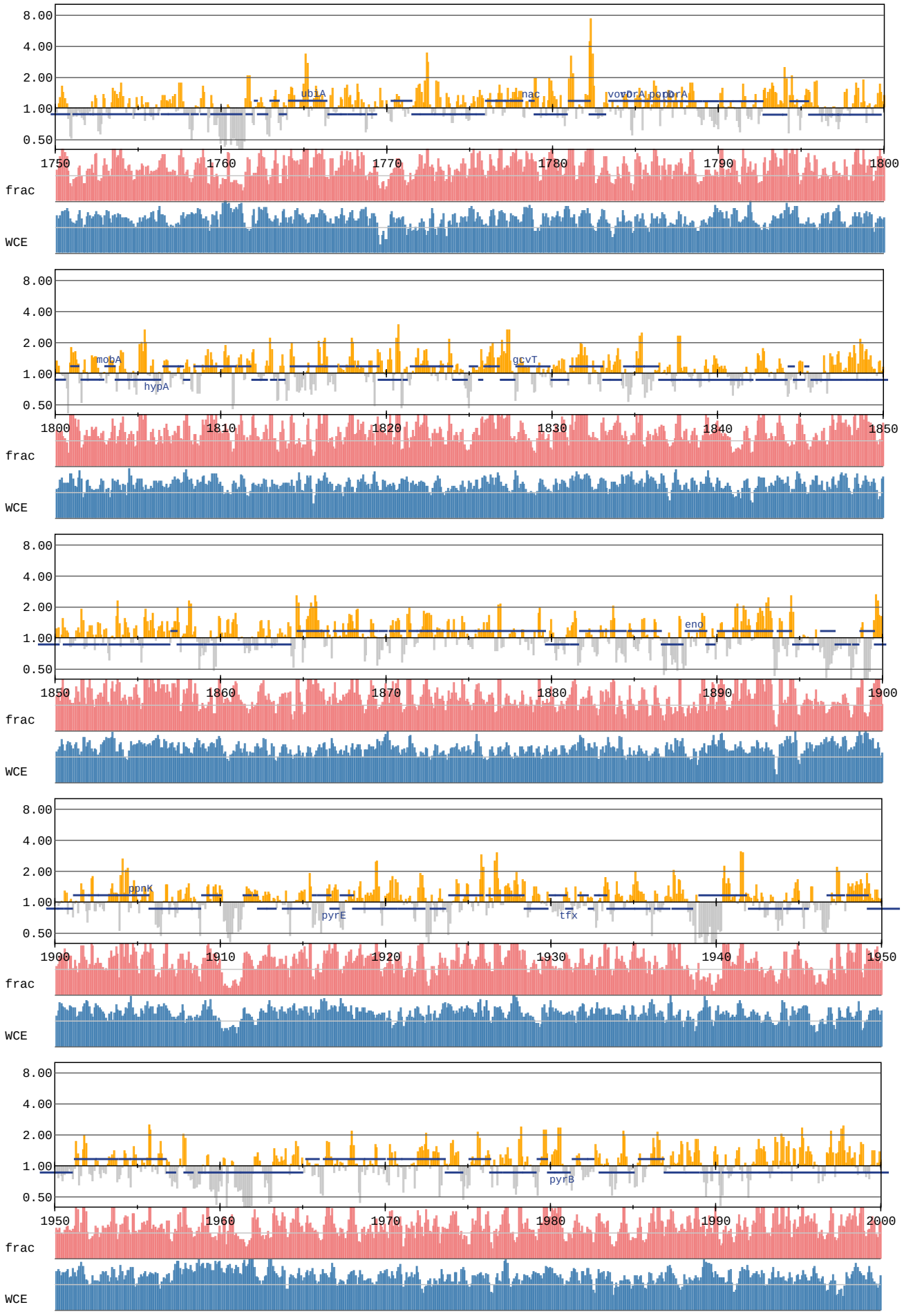
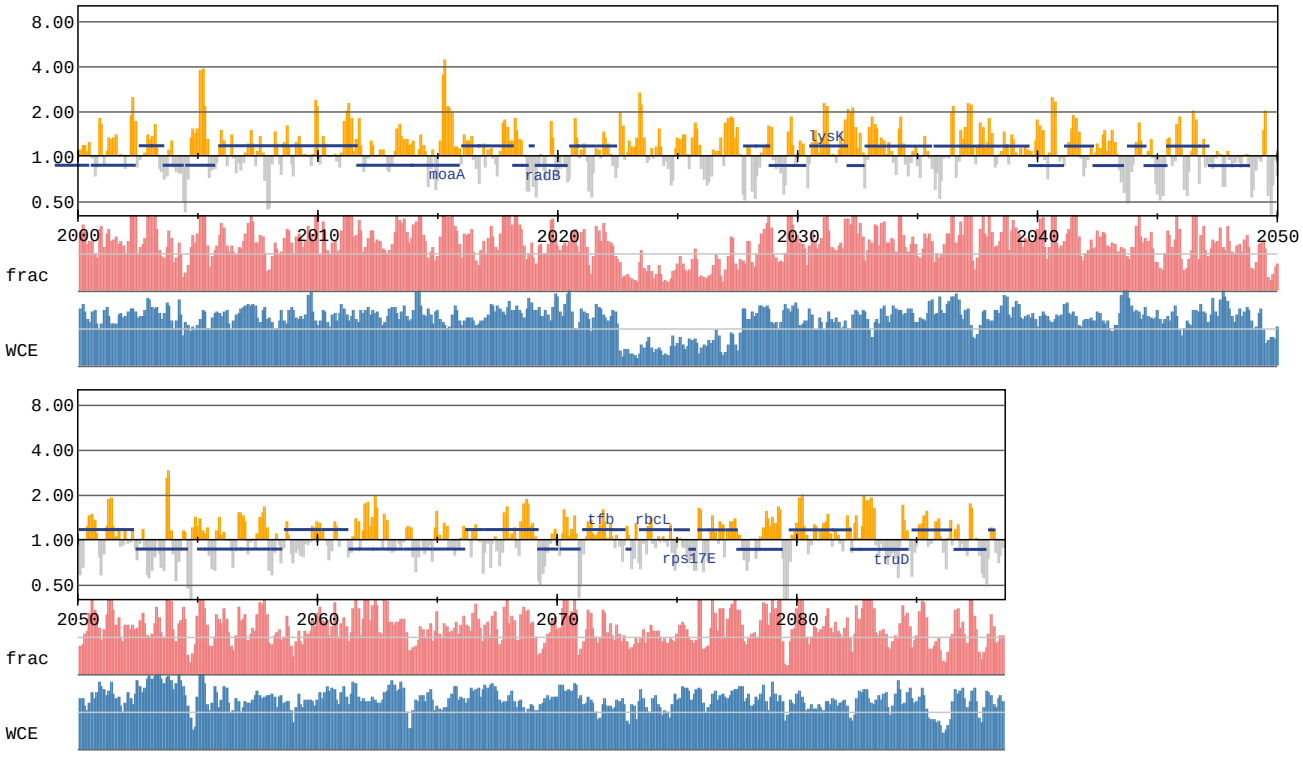
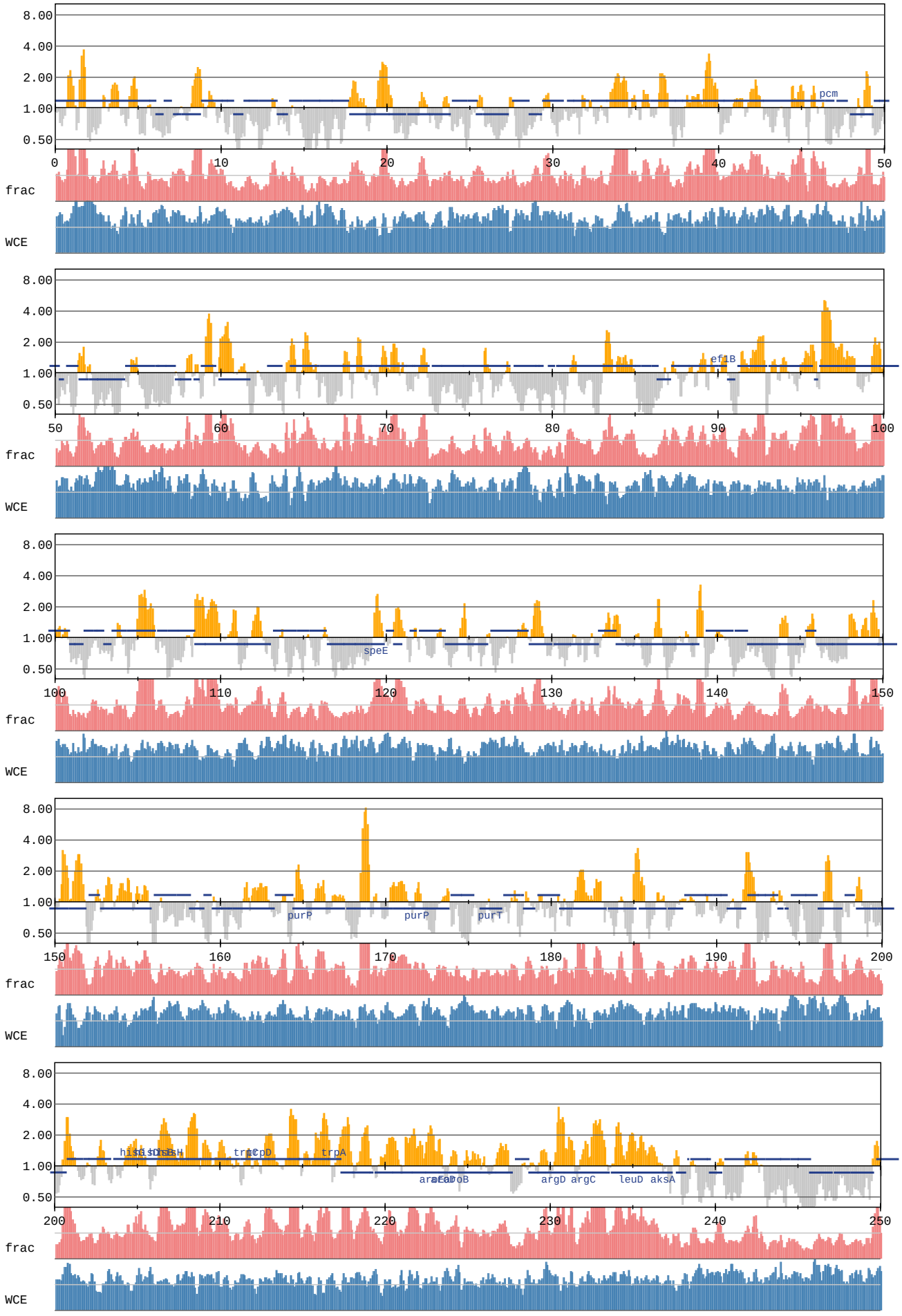


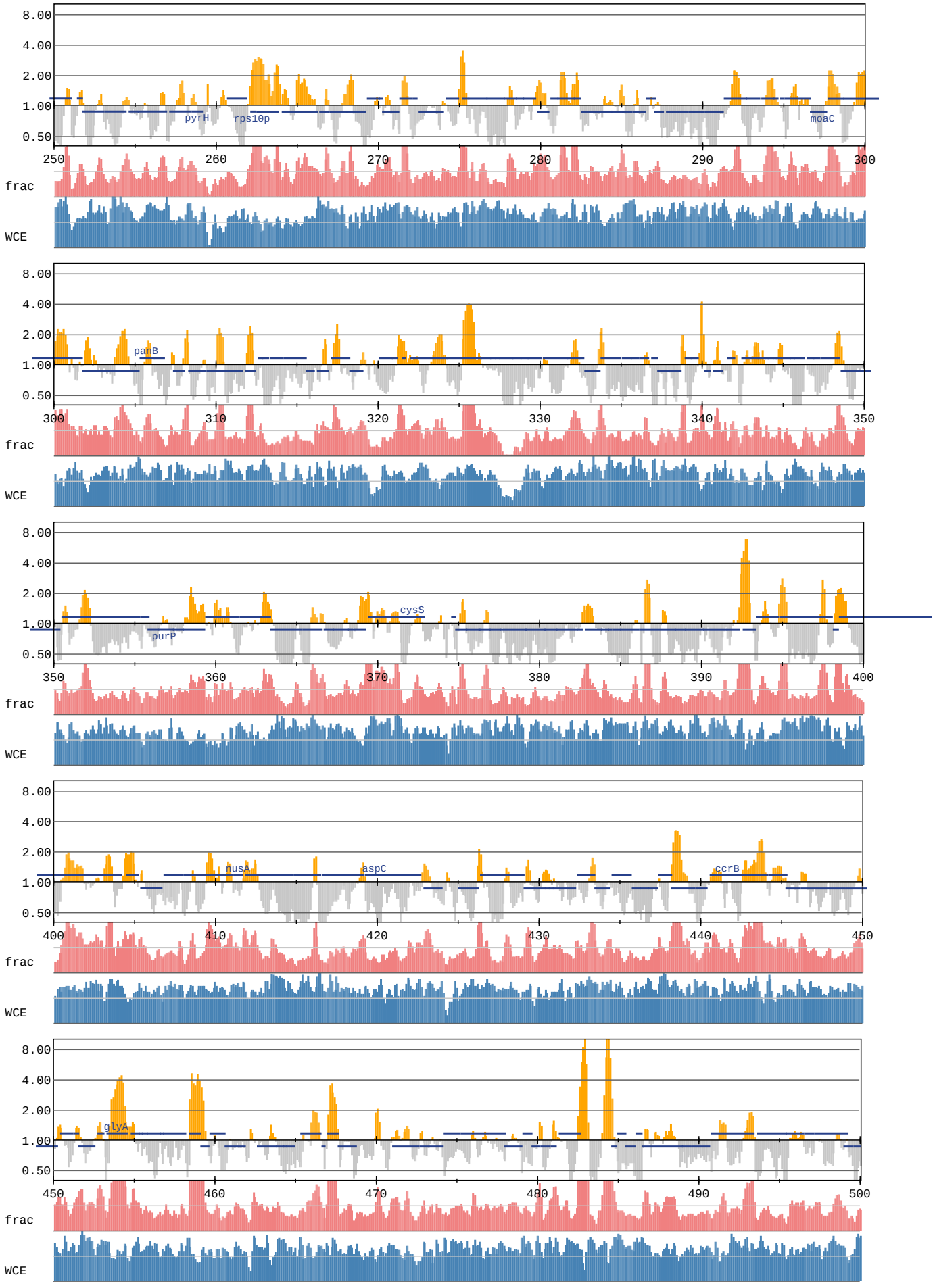
Histone-rich fraction



TK0471-rich fraction



TK0471-rich fraction



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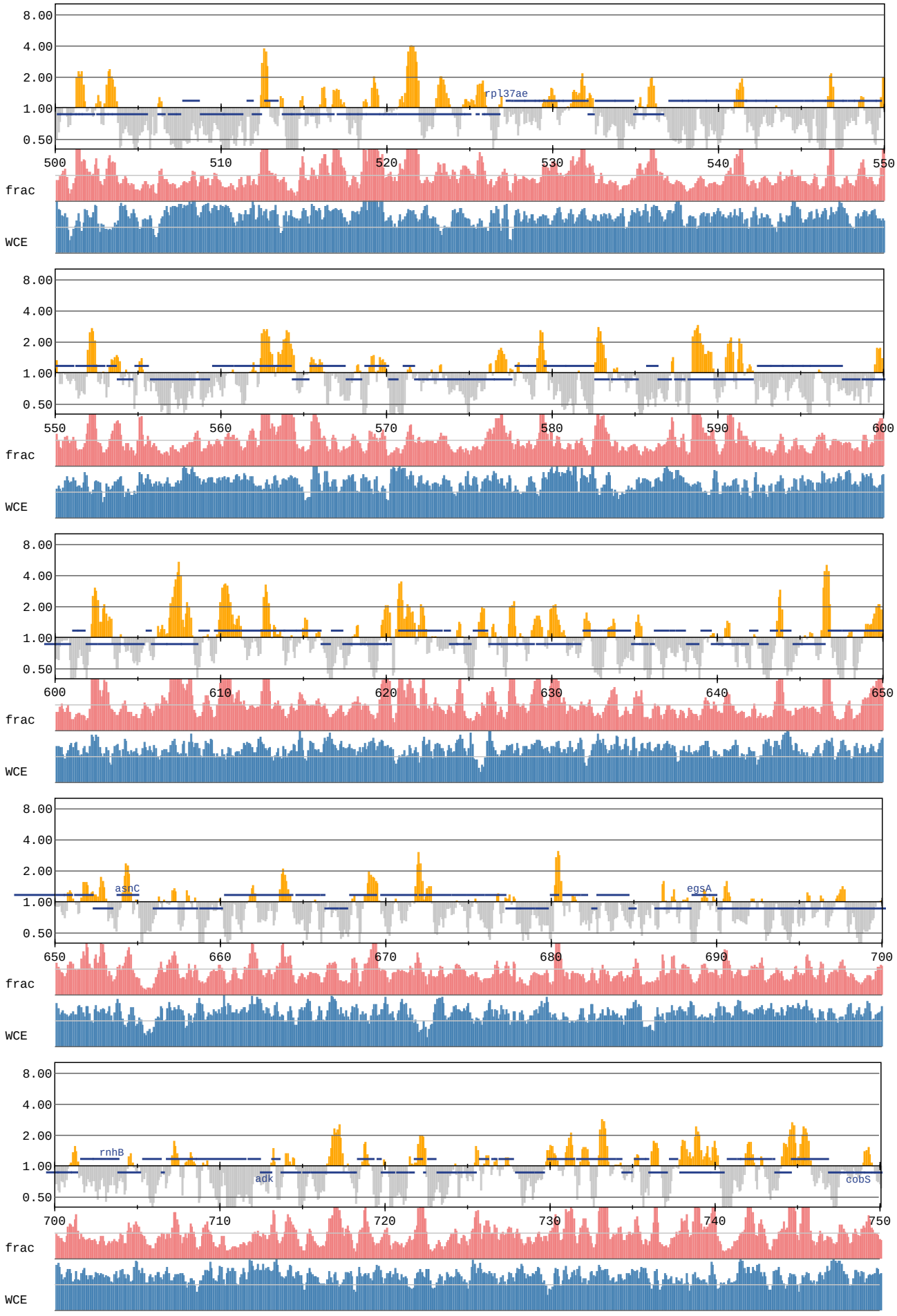

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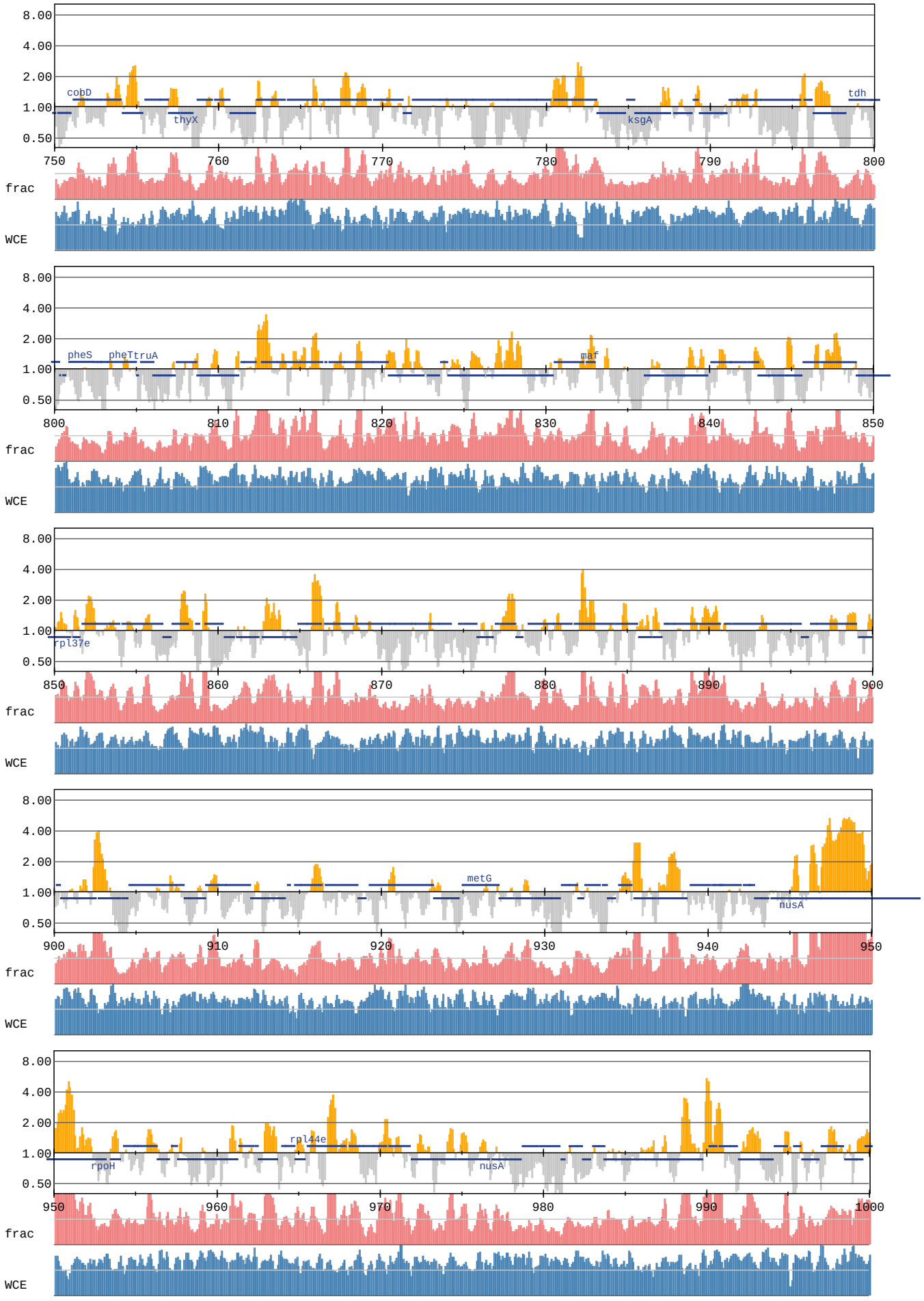

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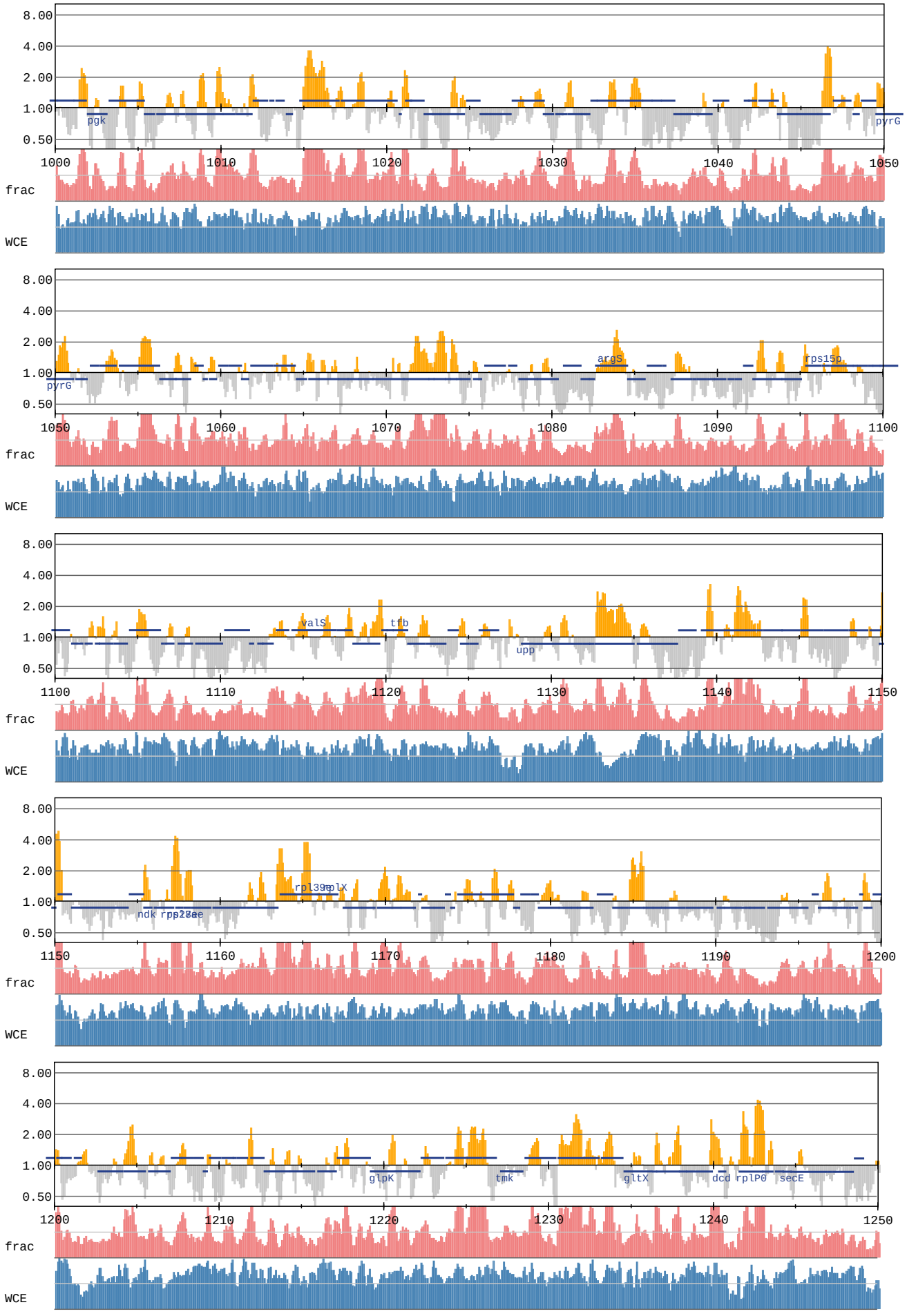

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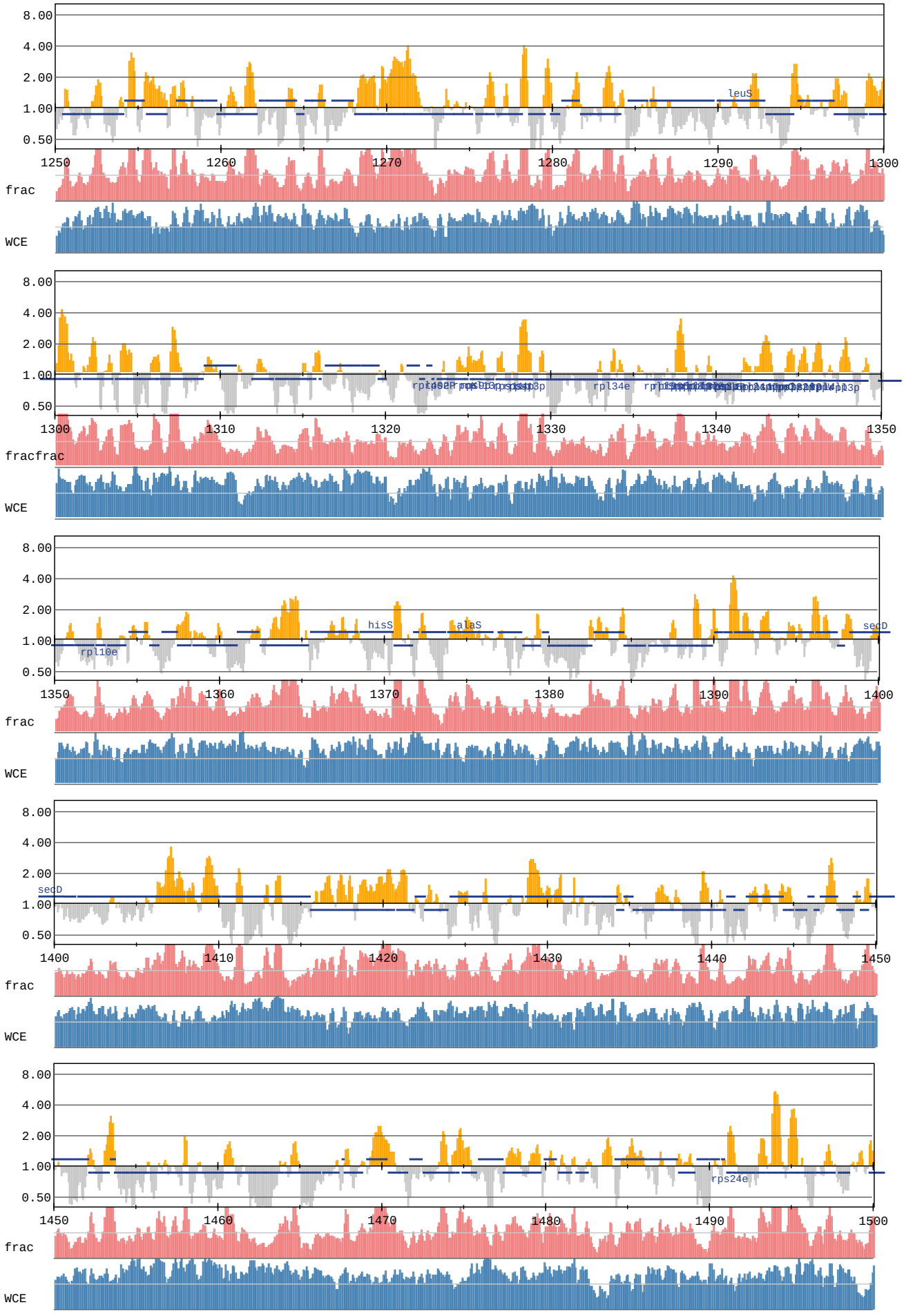
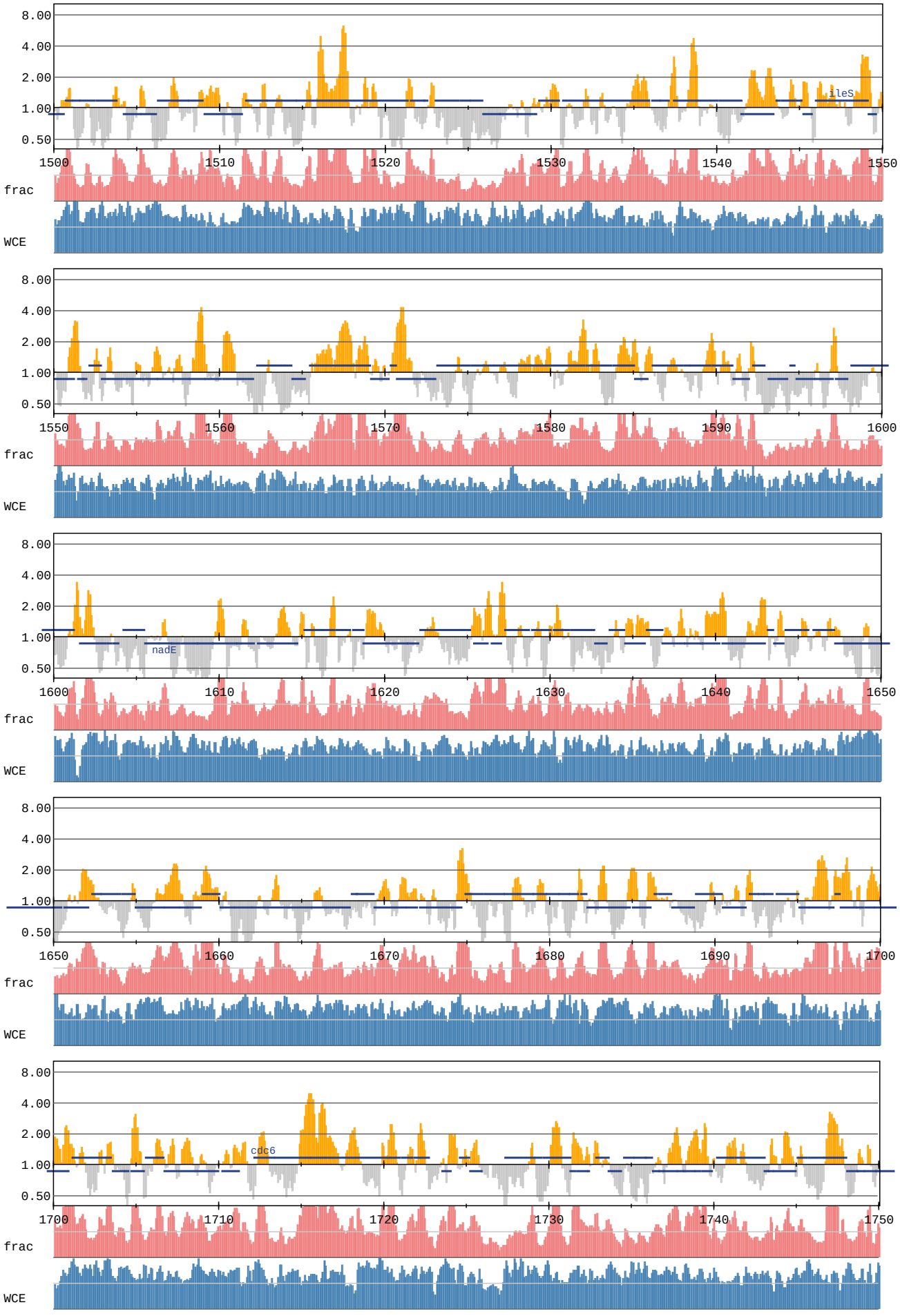


TK0471-rich fraction



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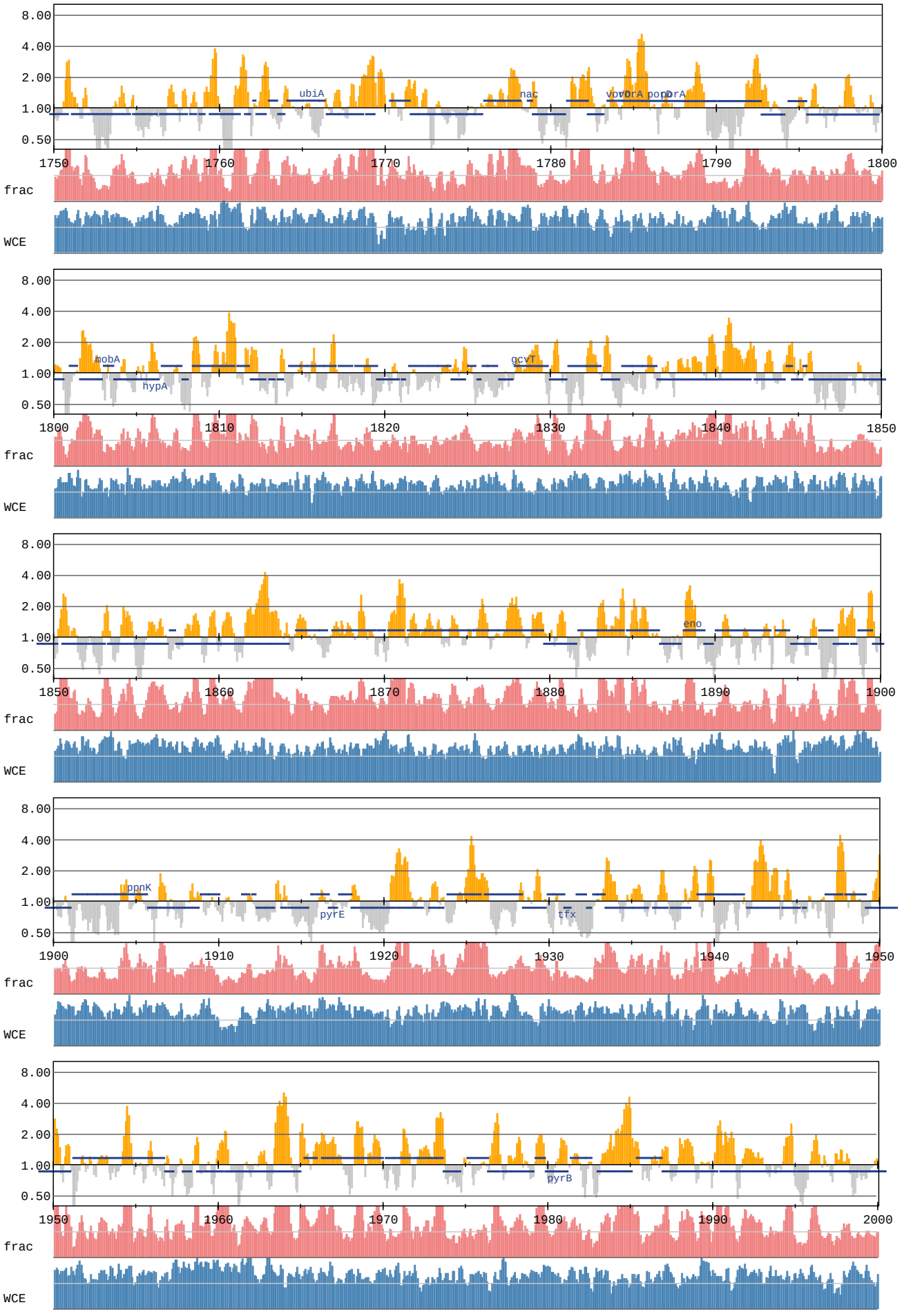

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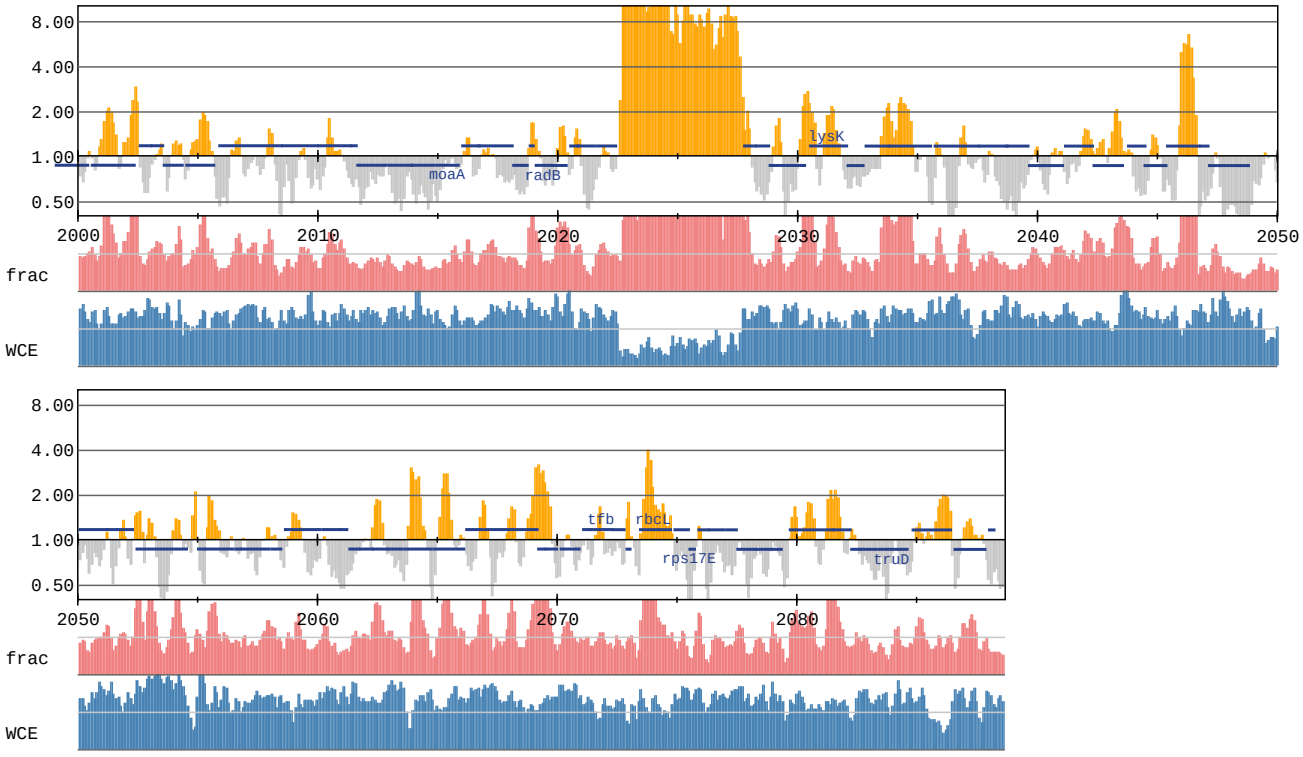

Appendix B. Genomic regions enriched with histone or TK0471/TrmBL2

Genomic regions enriched in the histone-rich light fraction (#3) and the TK0471-rich heavy fraction (#8) of the sucrose density gradient sedimentation of the MNase-digested chromatin fraction taken from *T. kodakarensis* KOD1 cells in the log phase or the stationary phase. The result of the log phase derives from massively parallel DNA sequencing, and the result of the stationary phase derives from Sanger sequencing of DNA cloned into a plasmid. In the log phase, the start and end positions of the genomic regions in each fraction that were enriched more than twofold are indicated, together with the middle position. In the stationary phase, the start and end positions of the cloned regions are indicated together with the middle position. Nucleotide numbering is according to the NCBI Reference Sequence: "NC_006624.1".

Appnedix B: Genomic regions enriched with histone or TK0471in the log and stationary phases

Log phase					
Histone-rich light fraction			TK0471-rich heavy fraction		
start	end	middle	start	end	middle
13192	13476	13334	683	953	818
18038	18287	18163	1499	1833	1666
19410	19663	19537	4679	4834	4757
20827	20994	20911	8392	8768	8580
22666	22872	22769	19537	20035	19786
31725	31886	31806	33728	34057	33893
34732	34893	34813	34227	34391	34309
47248	47539	47394	36439	36811	36625
47747	47914	47831	39190	39566	39378
48753	49041	48897	48877	49088	48983
63150	63359	63255	59023	59478	59251
63526	63649	63588	59897	60648	60273
65321	65532	65427	64195	64365	64280
68038	68155	68097	65031	65283	65157
70672	70789	70731	68199	68489	68344
72916	73039	72978	83183	83517	83350
83558	83811	83685	92370	92822	92596
84688	84896	84792	96251	97043	96647
90695	90815	90755	99463	99583	99523
94080	94198	94139	99713	99839	99776
99085	99208	99147	105016	105512	105264
99883	100000	99942	105679	105849	105764
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111904	112027	111966	109314	109768	109541
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117034	117155	117095	119328	119534	119431
121704	121872	121788	120663	120789	120726
125673	126002	125838	124673	124796	124735
136442	136562	136502	128926	129302	129114
140865	141030	140948	136354	136562	136458
156524	156764	156644	138862	139067	138965
167659	167867	167763	149375	149542	149459
168533	168656	168595	150378	150754	150566
172335	172584	172460	151138	151631	151385
185441	185562	185502	164529	164779	164654
186439	186562	186501	168533	169035	168784
192077	192197	192137	181684	182012	181848
199883	200003	199943	185063	185395	185229
203805	203966	203886	191737	192197	191967
206140	206260	206200	196583	197040	196812
212024	212482	212253	200631	200965	200798
216656	216779	216718	206307	206979	206643
216908	217028	216968	208017	208648	208333
217917	218038	217978	212693	213153	212923
222168	222291	222230	214151	214535	214343
229718	230012	229865	215703	215861	215782
237721	238029	237875	216028	216530	216279
242062	242323	242193	217325	217870	217598
242731	243030	242881	218662	218997	218830
244224	244535	244380	221543	221874	221709
255516	255642	255579	222543	223001	222772
276182	276384	276283	230346	230892	230619
295968	296091	296030	232561	233186	232874
298724	298930	298827	233937	234315	234126
301293	301317	301305	234729	235069	234899
302880	303129	303005	235427	235829	235628
311018	311270	311144	262152	262985	262569
315196	315487	315342	263159	263288	263224
323419	323545	323482	263538	263866	263702
326411	326672	326542	265040	265163	265102
330331	330554	330443	268214	268381	268298
341927	342196	342062	275057	275392	275225
345680	345830	345755	281238	281534	281386
346935	347205	347070	282200	282326	282263
366396	366528	366462	291889	292224	292057
368399	368531	368465	297776	298111	297944
371912	372029	371971	299613	300032	299823
379179	379372	379276	300126	300751	300439
388947	389176	389062	304136	304465	304301
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400378	400501	400440	310023	310349	310186
403003	403129	403066	311901	312276	312089
413891	414026	413959	317328	317536	317432
421191	421372	421282	321214	321370	321292
424900	425044	424972	323705	324007	323856
436416	436566	436491	325207	326013	325610
454167	454628	454398	333687	333901	333794
455170	455463	455317	338727	338915	338821
459891	460018	459955	339853	340211	340032
470915	471038	470977	348246	348601	348424
472164	472372	472268	351795	352001	351898
472836	473041	472939	358387	358513	358450
477176	477299	477238	362898	363153	363026
483686	483894	483790	369334	369487	369411
491572	491824	491698	386454	386808	386631
493208	493413	493311	392385	393027	392706
494375	494540	494458	394887	395198	395043
496962	497085	497024	397392	397700	397546
497754	498044	497899	398395	398827	398611

Stationary phase					
Histone-rich light fraction			TK0471-rich heavy fraction		
start	end	middle	start	end	middle
4479	4612	4546	25124	25461	25293
35860	36025	35943	26554	26767	26661
38020	38220	38120	39785	40208	39997
58543	58657	58600	56485	56795	56640
78793	78980	78887	69934	70214	70074
88729	88889	88809	76021	76463	76242
94105	94238	94172	79212	79615	79414
110453	110626	110540	86622	86902	86762
111689	111894	111792	90714	91082	90898
116597	116737	116667	101706	101908	101807
131186	131290	131238	108546	108868	108707
132851	133047	132949	111563	112064	111814
137955	138013	137984	114578	115001	114790
163502	163750	163626	125234	125639	125437
164448	164565	164507	132406	132700	132553
167892	168111	168002	147893	148183	148038
208497	208594	208546	156996	157089	157043
210558	210722	210640	167135	167312	167224
212955	213063	213009	184957	185300	185129
215196	215431	215314	186350	186896	186623
240968	241107	241038	193673	193954	193814
246099	246251	246175	228475	228797	228636
263125	263417	263271	237678	238045	237862
293831	294043	293937	275071	275283	275177
295466	295583	295525	285763	286016	285890
310528	310582	310555	291439	292026	291733
330230	330453	330342	291883	292202	292043
358567	358792	358680	347414	347862	347638
358969	359128	359049	368231	368489	368360
406016	406207	406112	373529	373603	373566
422394	422701	422548	386492	386805	386649
427158	427335	427247	429131	429355	429243
449643	449861	449752	469994	470184	470089
456134	456235	456185	475268	475442	475355
456510	456622	456566	502102	502343	502223
478782	478932	478857	519654	519815	519735
519684	519846	519765	541428	541699	541564
526030	526302	526166	560443	560711	560577
526784	526910	526847	563733	564011	563872
527158	527367	527263	611534	611838	611686
527284	527468	527376	611589	612034	611812
540311	540422	540367	648928	649177	649053
541428	541556	541492	661742	662106	661924
544432	544565	544499	670462	670747	670605
582668	582863	582766	670640	670856	670748
583687	583783	583735	672317	672506	672412
590678	590833	590756	691522	691942	691732
608316	608458	608387	707101	707354	707228
640513	640626	640570	735135	735327	735231
657865	657953	657909	817275	817769	817522
669205	669433	669319	831465	831795	831630
674673	674896	674785	843333	843584	843459
734075	734133	734104	847456	847861	847659
771798	772144	771971	897791	898064	897928
773247	773487	773367	904696	905111	904904
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843734	843854	843794	911696	912257	911977
851227	851417	851322	915507	915695	915601
872826	873066	872946	951517	951823	951670
881395	881520	881458	981557	981754	981656
895173	895455	895314	1015740	1016221	1015981
937192	937387	937290	1024115	1024741	1024428
951230	951402	951316	1042093	1042340	1042217
962721	962932	962827	1103861	1104160	1104011
1012538	1012690	1012614	1104485	1104762	1104624
1047467	1047598	1047533	1104670	1104962	1104816
1092154	1092280	1092217	1107834	1108106	1107970
1095090	1095218	1095154	1134046	1134591	1134319
1113768	1114007	1113888	1149916	1150141	1150029
1120292	1120551	1120422	1188690	1189046	1188868
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1145890	1146049	1145970	1219853	1219969	1219911
1148679	1148846	1148763	1256301	1256510	1256406
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1163135	1163211	1163173	1276323	1276566	1276445
1169621	1169737	1169679	1298626	1299403	1299015
1233233	1233359	1233296	1314548	1314823	1314686
1241652	1241765	1241709	1355534	1355953	1355744
1255619	1255793	1255706	1389874	1390133	1390004
1269259	1269501	1269380	1395972	1396276	1396124
1270582	1270848	1270715	1491140	1491353	1491247
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1345816	1345969	1345893	1574246	1574629	1574438
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1367884	1367979	1367932	1586846	1587086	1586966

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523539	523665	523602	438222	438833	438528
533723	534013	533868	443564	444051	443808
540569	540821	540695	453502	454468	453985
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545745	545909	545827	466034	466157	466096
546574	546700	546637	467037	467562	467300
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551500	551627	551564	482573	483068	482821
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573539	573662	573601	512394	512851	512623
578422	578545	578484	519155	519281	519218
591234	591527	591381	521159	521872	521516
603297	603461	603379	523164	523369	523267
610685	610849	610767	531719	531883	531801
625711	626004	625858	546703	546911	546807
630341	630508	630425	552002	552459	552231
631428	631678	631553	562394	562977	562686
632721	632888	632805	563689	564146	563918
635059	635309	635184	579216	579506	579361
639066	639315	639191	582677	583052	582865
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656175	656342	656259	590692	590900	590796
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677671	677879	677775	607889	608138	608014
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708308	708637	708473	620658	621036	620847
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719155	719278	719217	622036	622288	622162
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743447	743699	743573	627422	627794	627608
753675	753842	753759	630051	630300	630176
769202	769366	769284	643696	643907	643802
771162	771288	771225	646372	646911	646642
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827838	828005	827922	744452	744822	744637
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1865348	1865597	1865473	1952649	1953053	1952851
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1897397	1897568	1897483	1959334	1959510	1959422
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1210182	1210473	1210328	1155301	1155509	1155405
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1276676	1276797	1276737	1220412	1220532	1220472
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1296583	1296829	1296706	1225167	1225542	1225355
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1326674	1327005	1326840	1233555	1233807	1233681
1333678	1333807	1333743	1236431	1236560	1236496
1338731	1338898	1338815	1237686	1237897	1237792
1339355	1339567	1339461	1239730	1240067	1239899
1339736	1340026	1339881	1241571	1242069	1241820
1347245	1347544	1347395	1242362	1243075	1242719
1353505	1353754	1353630	1254385	1254845	1254615
1359516	1359640	1359578	1255387	1255633	1255510
1360516	1360645	1360581	1255803	1255973	1255888
1361893	1362022	1361958	1261521	1261981	1261751
1369408	1369534	1369471	1268409	1268655	1268532
1369698	1369991	1369845	1269162	1269282	1269222
1373206	1373373	1373290	1269663	1269868	1269766
1374710	1374874	1374792	1270038	1271791	1270915
1376920	1377172	1377046	1276166	1276386	1276276
1377837	1378007	1377922	1278171	1278511	1278341
1384431	1384809	1384620	1279555	1279886	1279721
1388356	1388526	1388441	1281351	1281553	1281452
1388731	1388901	1388816	1283227	1283561	1283394
1392362	1392535	1392449	1292072	1292409	1292241
1407137	1407345	1407241	1294452	1294824	1294638
1416152	1416360	1416256	1299083	1299215	1299149
1423705	1423875	1423790	1300170	1300753	1300462
1434229	1434516	1434373	1302169	1302462	1302316
1448962	1449077	1449020	1307013	1307351	1307182
1453174	1453338	1453256	1328048	1328549	1328299
1465695	1465982	1465839	1337562	1338022	1337792
1467154	1467359	1467257	1342737	1343200	1342969
1471835	1472034	1471935	1346076	1346208	1346142
1473540	1473787	1473664	1347705	1347913	1347809
1498203	1498417	1498310	1363690	1364024	1363857
1501792	1502001	1501897	1364188	1364771	1364480
1507513	1507639	1507576	1370533	1370996	1370765
1533431	1533554	1533493	1384349	1384519	1384434
1533933	1534182	1534058	1388690	1389068	1388879
1534561	1534681	1534621	1389853	1390026	1389940
1540196	1540319	1540258	1390859	1391404	1391132
1545204	1545327	1545266	1395953	1396331	1396142
1548081	1548331	1548206	1406679	1407263	1406971
1553297	1553465	1553381	1407515	1407638	1407577
1559015	1559264	1559140	1409141	1409642	1409392
1560141	1560268	1560205	1411149	1411354	1411252
1561517	1561643	1561580	1420158	1420492	1420325
1564190	1564480	1564335	1421035	1421369	1421202
1566818	1566988	1566903	1428842	1429505	1429174
1567153	1567276	1567215	1439364	1439563	1439464
1567904	1568156	1568030	1447084	1447412	1447248
1568904	1569030	1568967	1453174	1453631	1453403
1569702	1570033	1569868	1457887	1458013	1457950
1571201	1571368	1571285	1469534	1470158	1469846
1572706	1573037	1572872	1473666	1473872	1473769
1576170	1576291	1576231	1474669	1474874	1474772
1576420	1576792	1576606	1491073	1491524	1491299
1578922	1579172	1579047	1493740	1494326	1494033
1583724	1584018	1583871	1494865	1495328	1495097

1588691	1588899	1588795	1515900	1516361	1516131
1593074	1593197	1593136	1517153	1517778	1517466
1593869	1594033	1593951	1535182	1535306	1535244
1605175	1605465	1605320	1535558	1535684	1535621
1609807	1609974	1609891	1537227	1537562	1537395
1612521	1612773	1612647	1538354	1538896	1538625
1616525	1616654	1616590	1542071	1542405	1542238
1617320	1617528	1617424	1542945	1543320	1543133
1624833	1624997	1624915	1548706	1549331	1549019
1629213	1629506	1629360	1551000	1551502	1551251
1632847	1633015	1632931	1558513	1559015	1558764
1633848	1634056	1633952	1560185	1560766	1560476
1638354	1638565	1638460	1567153	1568030	1567592
1643364	1643573	1643469	1568655	1568863	1568759
1660520	1660766	1660643	1570532	1571283	1570908
1675417	1675543	1675480	1581718	1582178	1581948
1680049	1680383	1680216	1584349	1584555	1584452
1680550	1680676	1680613	1584933	1585180	1585057
1681216	1681510	1681363	1589691	1589900	1589796
1685224	1685394	1685309	1592071	1592197	1592134
1687060	1687312	1687186	1597081	1597328	1597205
1688688	1688814	1688751	1601168	1601499	1601334
1692695	1692822	1692759	1601877	1602253	1602065
1693866	1694030	1693948	1609892	1610141	1610017
1694368	1694535	1694452	1613814	1613979	1613897
1695450	1695573	1695512	1616695	1617027	1616861
1695952	1696327	1696140	1626165	1626502	1626334
1697372	1697580	1697476	1626919	1627294	1627107
1699736	1699918	1699827	1630342	1630509	1630426
1706636	1706844	1706740	1640237	1640569	1640403
1708889	1709138	1709014	1642695	1643071	1642883
1709514	1709640	1709577	1651666	1652001	1651834
1721160	1721283	1721222	1656870	1657510	1657190
1724331	1724498	1724415	1659015	1659264	1659140
1730844	1731008	1730926	1674413	1674874	1674644
1739442	1739694	1739568	1681718	1681885	1681802
1741237	1741528	1741383	1683056	1683387	1683222
1742197	1742320	1742259	1684848	1685180	1685014
1743364	1743907	1743636	1692068	1692194	1692131
1761517	1761769	1761643	1696204	1696829	1696517
1765027	1765277	1765152	1697245	1697410	1697328
1772327	1772538	1772433	1697873	1698079	1697976
1781052	1781301	1781177	1699457	1699580	1699519
1782181	1782512	1782347	1700625	1700956	1700791
1793947	1794073	1794010	1704673	1705131	1704902
1794363	1794533	1794448	1712521	1712770	1712646
1805138	1805261	1805200	1714900	1715859	1715380
1805299	1805508	1805404	1716026	1716525	1716276
1812892	1813015	1812954	1717904	1718279	1718092
1814194	1814359	1814277	1720324	1720658	1720491
1815819	1815983	1815901	1722034	1722369	1722202
1816156	1816356	1816256	1723912	1724161	1724037
1817822	1818030	1817926	1724208	1724372	1724290
1820594	1820781	1820688	1730175	1730674	1730425
1823705	1823869	1823787	1731427	1731551	1731489
1826075	1826497	1826286	1737565	1737811	1737688
1826917	1827046	1826982	1738729	1739025	1738877
1827213	1827500	1827357	1739357	1739565	1739461
1831682	1831800	1831741	1744238	1744532	1744385
1835228	1835515	1835372	1746873	1747580	1747227
1837562	1837815	1837689	1750669	1751000	1750835
1848581	1848707	1848644	1759394	1759848	1759621
1853672	1853839	1853756	1761185	1761643	1761414
1857302	1857470	1857386	1762523	1762980	1762752
1858012	1858261	1858137	1768532	1769368	1768950
1864526	1864775	1864651	1769535	1769866	1769701
1865400	1865857	1865629	1777547	1778005	1777776
1871324	1871491	1871408	1781219	1781386	1781303
1876708	1877002	1876855	1781844	1782052	1781948
1879213	1879383	1879298	1782181	1782386	1782284
1883676	1883806	1883741	1784433	1784891	1784662
1891070	1891316	1891193	1785184	1785894	1785539
1891568	1891692	1891630	1788688	1789067	1788878
1892568	1892692	1892630	1792196	1792698	1792447
1892947	1893193	1893070	1797871	1798079	1797975
1894448	1894569	1894509	1801628	1801997	1801813
1899578	1899833	1899706	1805801	1805965	1805883
1904006	1904132	1904069	1808388	1808763	1808576
1904173	1904493	1904333	1810391	1811018	1810705
1919321	1919529	1919425	1816819	1817024	1816922
1925705	1926002	1925854	1830222	1830506	1830364
1926538	1926793	1926666	1832345	1832553	1832449
1927834	1928005	1927920	1833345	1833553	1833449
1935052	1935184	1935118	1839565	1839900	1839733
1937348	1937518	1937433	1840565	1841023	1840794
1940436	1940565	1940501	1842067	1842193	1842130
1941436	1941695	1941566	1844572	1844695	1844634
1947237	1947539	1947388	1850501	1850748	1850625
1951669	1951833	1951751	1853129	1853255	1853192
1955634	1955842	1955738	1854132	1854258	1854195
1957681	1957842	1957762	1861813	1861977	1861895
1967904	1968025	1967965	1862188	1863021	1862605

1972412	1972532	1972472	1868529	1868655	1868592
1975544	1975664	1975604	1870702	1871283	1870993
1978169	1978289	1978229	1875817	1876043	1875930
1979550	1979794	1979672	1877544	1878046	1877795
1980424	1980670	1980547	1882926	1883304	1883115
1984348	1984550	1984449	1884225	1884553	1884389
1986436	1986556	1986496	1885058	1885304	1885181
1993821	1994073	1993947	1885559	1885806	1885683
1995190	1995322	1995256	1888187	1888683	1888435
1996944	1997076	1997010	1888730	1888891	1888811
1997572	1997830	1997701	1898249	1898408	1898329
2002170	2002337	2002254	1899249	1899578	1899414
2005007	2005342	2005175	1920655	1921494	1921075
2009808	2010014	2009911	1925040	1925544	1925292
2011144	2011353	2011249	1929213	1929380	1929297
2015149	2015525	2015337	1933424	1933679	1933552
2023331	2023539	2023435	1936721	1937020	1936871
2031054	2031300	2031177	1938727	1939023	1938875
2032055	2032178	2032117	1939683	1939897	1939790
2032219	2032387	2032303	1942354	1943196	1942775
2036436	2036563	2036500	1943566	1943903	1943735
2037062	2037311	2037187	1944357	1944530	1944444
2040565	2040818	2040692	1947363	1947912	1947638
2046453	2046576	2046515	1949868	1950422	1950145
2049460	2049583	2049522	1954299	1954631	1954465
2053630	2053838	2003734	1960309	1960514	1960412
2062313	2062477	2012395	1963397	1964274	1963836
2080176	2080299	2030238	1964898	1965148	1965023
2082722	2082889	2032806	1966194	1966482	1966338
			1968198	1968778	1968488
			1969409	1969529	1969469
			1971160	1971365	1971263
			1973163	1973658	1973411
			1976670	1977040	1976855
			1979424	1979667	1979546
			1983720	1983882	1983801
			1984055	1985052	1984554
			1990193	1990560	1990377
			1990689	1990818	1990754
			1991061	1991190	1991126
			1994692	1994824	1994758
			1996193	1996325	1996259
			2001128	2001333	2001231
			2002170	2002502	2002336
			2022538	2027794	2025166
			2027838	2028006	2027922
			2030176	2030549	2030363
			2031344	2031550	2031447
			2033682	2033887	2033785
			2034181	2034680	2034431
			2043237	2043405	2043321
			2045951	2046576	2046264
			2054798	2054966	2004882
			2055383	2055506	2005445
			2063813	2064271	2014042
			2065149	2065522	2015336
			2068905	2069657	2019281
			2073662	2074038	2023850
			2081344	2081512	2031428
			2081553	2081676	2031615
			2086060	2086310	2036185

Appendix C. Complete result of microarray analysis

A pair ("left" and "right") of signal intensity ratio (Log_2[KCP1/KUW1]) and the mean ± s.d. value of each ORF in the log and the stationary phase is indicated. ORFs that exhibited TK0471 enrichment on the promoter region (-200 to +50) are labeled as "5'", together with the position of the enrichment peak (middle position of the enriched region) relative to the predicted translation start site (start codon) of each ORF. ORFs that belong to the same predicted operon with an ORF with TK0471 enrichment on the promoter are labeled as "operon". ORFs that exhibit TK0471 enrichment on the coding region (+50 to stop codon) are labeled as "coding".

Appendix C: Complete result of microarray analysis

Gene ID	Annotation	Log_2(KCP1/KUW1)								TK0471 position	
		Log phase				Stationary phase					
		Left ratio	Right ratio	Mean	SD	Left ratio	Right ratio	Mean	SD	Log	Statinary
TK0001	DNA-directed DNA polymerase, family B; two i	-1.01	-0.95	-0.98	0.04	0.06	0.31	0.19	0.18	coding	
TK0002	Predicted zinc-dependent protease, DUF45 far	-0.32	-0.44	-0.38	0.08	-1.29	-0.99	-1.14	0.21		
TK0003	Hypothetical membrane protein, conserved_CO	-0.61	-0.59	-0.60	0.02	-	-0.23	-	-		
TK0004	Hypothetical membrane protein, conserved	0.27	0.21	0.24	0.04	-0.59	-0.84	-0.71	0.18		
TK0005	CoA-binding protein_COG1832	-0.06	-0.20	-0.13	0.10	1.12	-0.40	0.36	1.07		
TK0006	Hypothetical protein, conserved	-0.47	-0.01	-0.24	0.33	-	-	-	-		
TK0007	Hypothetical protein, conserved	0.31	0.28	0.29	0.02	-	0.60	-	-		
TK0008	Predicted DNA methylase_COG1041	-0.03	0.30	0.14	0.23	-	1.20	-	-	coding	
TK0009	Hypothetical protein, conserved	-0.30	-0.22	-0.26	0.06	0.87	0.24	0.56	0.44		
TK0010	Hypothetical protein	0.78	0.52	0.65	0.18	-	4.37	-	-		
TK0011	Hypothetical protein, conserved, UPF0047 fami	0.72	0.44	0.58	0.20	0.84	0.03	0.43	0.58		
TK0012	GTP-binding protein_COG1100	-0.49	-0.32	-0.41	0.13	-	2.28	-	-		
TK0013	Hypothetical protein, conserved	-0.79	-0.33	-0.56	0.32	0.75	0.66	0.71	0.06		
TK0014	Metal-dependent phosphohydrolase, HD superf	-0.55	-0.34	-0.45	0.15	-	-0.21	-	-		
TK0015	ABC-type molybdate transport system, peripla	-0.20	-0.15	-0.18	0.03	-1.27	-1.32	-1.30	0.04		
TK0016	Predicted nucleic acid-binding protein, containi	-0.59	-0.31	-0.45	0.20	1.20	2.68	1.94	1.05		
TK0017	Predicted transcription regulator, SpoVT/AbrB	-	-0.17	-	-	-	-	-	-		
TK0018	ABC-type sulfate transport system, permease	-0.43	-0.28	-0.35	0.10	0.16	1.68	0.92	1.08		
TK0019	Predicted ABC-type transport system, ATPase	-	-	-	-	-	-	-	-		
TK0020	Hypothetical protein, conserved	-0.01	-0.18	-0.10	0.12	-	1.39	-	-		
TK0021	ABC-type sulfate transport system, ATPase c	0.19	0.07	0.13	0.09	1.78	-	-	-		
TK0022	Hypothetical protein, conserved, Band 7 family	0.31	-0.07	0.12	0.27	-0.48	-0.19	-0.33	0.21		
TK0023	Hypothetical protein, conserved	0.93	0.91	0.92	0.02	0.16	1.39	0.77	0.87		
TK0024	Hypothetical protein, conserved	0.96	0.83	0.89	0.09	-0.75	0.68	-0.04	1.01	coding	
TK0025	Hypothetical membrane protein, conserved	-0.17	0.05	-0.06	0.15	1.32	0.93	1.13	0.28		
TK0026	Probable phosphoglycolate phosphatase, HAD	-0.16	-0.23	-0.19	0.05	-0.10	0.21	0.06	0.22		
TK0027	Hypothetical protein, conserved, UPF0066 fami	-0.31	-0.20	-0.25	0.07	-0.35	-0.30	-0.32	0.03		
TK0028	S-Adenosyl-L-homocysteine hydrolase_COG0	-0.74	-0.61	-0.67	0.10	-0.76	-1.92	-1.34	0.82		
TK0029	Zinc-dependent hydrolase, glyoxylase II family_	-0.35	-0.37	-0.36	0.01	-	0.93	-	-		
TK0030	Cyclase-related protein_COG1878	-0.06	-0.37	-0.22	0.22	-	-0.75	-	-		coding
TK0031	Ribonuclease P component, Rpp21 homolog_CO	-0.81	-0.57	-0.69	0.18	-	2.22	-	-		
TK0032	Hypothetical protein, conserved_COG1241	-0.01	-0.01	-0.01	0.00	-1.52	-0.57	-1.04	0.67		coding
TK0033	Hypothetical protein, conserved, containing leu	0.21	-0.05	0.08	0.18	-0.09	0.01	-0.04	0.07		
TK0034	Hypothetical protein, conserved	-0.56	-0.19	-0.37	0.26	0.41	1.57	0.99	0.82		
TK0035	Hypothetical membrane protein, conserved_CO	0.16	0.01	0.09	0.10	0.74	0.37	0.55	0.26		
TK0036	Hypothetical protein, conserved, DUF1495 fam	0.03	-0.02	0.01	0.03	0.46	0.82	0.64	0.25		
TK0037	SAM-dependent methyltransferase, UbiE/COQ	-0.29	-0.10	-0.20	0.13	-0.36	-0.15	-0.26	0.14		
TK0038	Archaeal flagellin B1 precursor_COG1681	-0.06	-0.66	-0.36	0.43	0.29	0.09	0.19	0.14		
TK0039	Archaeal flagellin B2 precursor_COG1681	-0.47	-0.60	-0.54	0.09	0.10	2.25	1.17	1.52	coding	
TK0040	Archaeal flagellin B3 precursor_COG1681	-0.27	-0.32	-0.30	0.04	0.41	0.08	0.25	0.24		
TK0041	Archaeal flagellin B4 precursor_COG1681	0.48	0.24	0.36	0.17	-0.46	-0.12	-0.29	0.24		
TK0042	Archaeal flagellin B5 precursor_COG1681	0.77	0.01	0.39	0.54	0.50	0.51	0.50	0.00	coding	
TK0043	Archaeal flagella-related protein C_COG3352	0.21	0.12	0.16	0.06	0.52	0.49	0.51	0.02		
TK0044	Archaeal flagella-related protein D, internal ins	-0.09	-0.41	-0.25	0.22	0.60	0.25	0.42	0.25		
TK0045	Archaeal flagella-related protein F_COG3353	0.21	0.01	0.11	0.14	-	-0.68	-	-	coding	
TK0046	Archaeal flagella-related protein G_COG3354	0.93	0.54	0.74	0.28	0.39	0.76	0.58	0.26		coding
TK0047	Archaeal flagella-related protein H, predicted A	0.09	-0.12	-0.02	0.15	-	0.32	-	-		
TK0048	Archaeal flagella-related protein I, predicted se	-0.36	-0.18	-0.27	0.13	1.38	0.32	0.85	0.75		
TK0049	Archaeal flagella-related membrane protein J,	-0.20	-0.16	-0.18	0.03	-0.63	-0.91	-0.77	0.20		
TK0050	Hypothetical membrane protein, conserved	-0.40	-0.10	-0.25	0.21	1.14	0.26	0.70	0.63		
TK0051	Protein-L-isoaspartate carboxylmethyltransfer	-0.42	-0.22	-0.32	0.14	-0.13	1.48	0.67	1.14		
TK0052	Phosphoserine phosphatase_COG0560	0.63	0.38	0.50	0.17	1.24	1.48	1.36	0.18		
TK0053	Archaeal signal peptidase, A24 family_COG1989	-	-0.51	-	-	-0.93	-1.29	-1.11	0.25	coding	
TK0054	Hypothetical protein, conserved	-0.83	-0.61	-0.72	0.16	1.10	1.80	1.45	0.49		
TK0055	Hypothetical protein, conserved, DUF1530 fam	-0.47	-0.34	-0.40	0.09	0.59	-	-	-		
TK0056	Hypothetical protein, conserved, DUF437 family	-0.33	-0.10	-0.22	0.16	0.12	0.65	0.39	0.38		
TK0057	Hypothetical protein	-0.46	-0.37	-0.41	0.07	1.21	0.97	1.09	0.17		
TK0058	Hydrolase, HAD superfamily_COG1011	-0.88	-0.63	-0.75	0.18	-0.59	2.41	0.91	2.12		
TK0059	CDP-alcohol phosphatidyltransferase_COG055	-0.01	-0.19	-0.10	0.13	-	0.58	-	-		
TK0060	Hypothetical protein, conserved, DUF127 family	-0.03	-0.15	-0.09	0.08	-1.09	-0.61	-0.85	0.34		
TK0061	Hypothetical protein, conserved	-0.82	-0.30	-0.56	0.37	-0.58	-0.35	-0.47	0.17		
TK0062	Hypothetical protein, conserved, DUF62 family_	-0.03	-0.28	-0.15	0.17	4.80	1.20	3.00	2.54		
TK0063	Nucleotidyltransferase, fused to N-terminal DN	0.06	0.02	0.04	0.02	-	0.53	-	-		
TK0064	Hypothetical protein, conserved, DUF103 family	0.25	-0.03	0.11	0.20	-	5.74	-	-		
TK0065	Hypothetical protein, conserved	-0.21	-0.31	-0.26	0.07	-	1.99	-	-		
TK0066	Predicted nucleic acid-binding protein, containi	-0.59	-0.57	-0.58	0.01	3.07	1.31	2.19	1.25		coding
TK0067	Nicotinamide mononucleotide adenylyltransfera	-0.48	-0.32	-0.40	0.11	0.63	0.70	0.67	0.05		
TK0068	Hypothetical membrane protein, conserved	0.31	0.09	0.20	0.15	1.70	-0.09	0.81	1.27		
TK0069	Predicted exonuclease, RecB family_COG1468	0.49	0.22	0.35	0.20	0.68	0.48	0.58	0.14		
TK0070	Hypothetical protein, conserved	-0.34	-0.41	-0.38	0.05	-0.51	-0.39	-0.45	0.08		
TK0071	Met-10+ like protein_COG2520	-	-0.33	-	-	-	-	-	-	coding	
TK0072	Tungsten-containing oxidoreductase_COG2414	-0.06	-0.22	-0.14	0.11	-	-	-	-	coding	
TK0073	SSV1 integrase homolog, C-fragment_COG434	-	-0.16	-	-	-	-	-	-		
TK0074	Hypothetical protein	-0.64	-0.59	-0.61	0.04	-	-	-	-	coding	
TK0075	Hypothetical protein	-0.17	-0.41	-0.29	0.17	-	0.18	-	-		
TK0076	Subtilisin-like serine protease precursor_COG1	-0.77	-0.79	-0.78	0.01	-	-0.79	-	-	coding	
TK0077	Hypothetical membrane protein	0.01	-0.16	-0.07	0.12	-	-	-	-		
TK0078	Hypothetical membrane protein	-0.88	-0.47	-0.68	0.29	-	-	-	-		
TK0079	Hypothetical membrane protein	0.14	-0.15	0.00	0.20	0.04	0.76	0.40	0.51		
TK0080	Hypothetical membrane protein	0.17	-0.32	-0.08	0.35	-	-0.90	-	-		coding
TK0081	Hypothetical protein	-2.20	-0.93	-1.56	0.90	-	-0.77	-	-		
TK0082	Hypothetical protein	0.10	0.02	0.06	0.06	-	2.26	-	-		
TK0083	Hypothetical membrane protein	0.01	-0.18	-0.09	0.13	-	-1.14	-	-		
TK0084	Hypothetical protein	0.14	0.00	0.07	0.10	-	-	-	-		
TK0085	Hypothetical membrane protein	-0.88	-0.53	-0.70	0.24	-	-0.70	-	-		

TK0086	Predicted transcription regulator, ArsR family	-1.39	-0.42	-0.91	0.69	-0.22	1.08	0.43	0.92		
TK0087	Hypothetical protein	-0.60	-0.63	-0.61	0.02	-	-1.08	-	-		
TK0088	Hypothetical membrane protein, conserved	0.31	-0.08	0.11	0.28	-	-0.45	-	-		
TK0089	Hypothetical protein	-0.09	0.77	0.34	0.61	-	-	-	-		
TK0090	Hypothetical protein	1.87	1.55	1.71	0.22	-	-0.16	-	-		coding
TK0091	Hypothetical protein	0.60	-0.03	0.28	0.45	2.72	3.58	3.15	0.61		
TK0092	Hypothetical membrane protein	-0.72	-0.32	-0.52	0.28	-	-	-	-		
TK0093	Hypothetical membrane protein	-0.23	-0.30	-0.26	0.05	-	-0.97	-	-		coding
TK0094	Transcription regulator, SpoVT/AbrB family	0.14	0.13	0.13	0.00	2.58	1.00	1.79	1.12		
TK0095	Hypothetical protein	-0.36	-0.39	-0.38	0.02	-	-	-	-		
TK0096	DNA replication licensing factor, MCM2/3/5 fa	-0.85	-0.60	-0.73	0.18	3.95	4.29	4.12	0.24		
TK0097	Hypothetical protein	-0.26	-0.24	-0.25	0.01	-	-	-	-	coding	
TK0098	Hypothetical protein	0.00	-0.16	-0.08	0.11	-	-	-	-		
TK0099	Hypothetical protein	0.31	0.13	0.22	0.13	-	1.93	-	-		
TK0100	Hypothetical protein	-	-0.64	-	-	-	-	-	-		
TK0101	Hypothetical protein	0.15	0.11	0.13	0.03	-	-	-	-		
TK0102	Hypothetical protein, conserved	-1.20	-0.50	-0.85	0.49	-	-	-	-		
TK0103	Hypothetical protein	0.25	-0.14	0.05	0.28	-	0.16	-	-		
TK0104	Probable integrase/recombinase	-0.01	-0.52	-0.26	0.36	-	-0.97	-	-		
TK0105	SSV1 integrase homolog, N-fragment	0.43	0.11	0.27	0.23	0.61	0.16	0.38	0.32		
TK0106	Diphthine synthase, methylase subunit_COG17	0.19	-0.05	0.07	0.17	-	-1.00	-	-		coding
TK0107	Manganese-dependent transcription regulator_	0.19	0.08	0.14	0.07	-	-1.03	-	-		
TK0108	Hypothetical membrane protein, conserved_CO	0.49	0.39	0.44	0.07	-0.04	0.64	0.30	0.48		
TK0109	Hypothetical protein, conserved	-0.73	-0.26	-0.49	0.34	-	1.27	-	-		
TK0110	Hydrolase, HAD superfamily_COG1011	0.16	-0.11	0.03	0.19	-	2.47	-	-		
TK0111	Predicted zinc-ribbon RNA-binding protein inv	0.19	-0.01	0.09	0.14	-	-	-	-		
TK0112	Translation elongation factor EF-1, beta subun	-0.21	-0.16	-0.19	0.03	-	0.29	-	-		
TK0113	Hypothetical protein, conserved	-0.61	-0.40	-0.51	0.15	-	-0.78	-	-		coding
TK0114	Hypothetical protein, conserved	-	-0.09	-	-	-	-	-	-		
TK0115	Sodium/proline symporter, SSF family_COG059	-0.01	-0.04	-0.02	0.02	1.61	1.82	1.71	0.15	coding	
TK0116	Proline dehydrogenase, alpha subunit (dye-link	0.49	0.25	0.37	0.17	-0.09	-1.09	-0.59	0.71		
TK0117	Proline dehydrogenase, beta subunit (dye-linke	-0.07	-0.11	-0.09	0.02	-	-1.99	-	-		
TK0118	Hypothetical protein	0.02	-0.11	-0.04	0.09	1.32	0.19	0.76	0.80		
TK0119	Proline dehydrogenase, alpha subunit (dye-link	-0.41	-0.42	-0.42	0.01	-0.89	-0.15	-0.52	0.52	coding	
TK0120	Proline dehydrogenase, gamma subunit (4Fe-4	-0.16	-0.22	-0.19	0.05	-0.27	-0.42	-0.34	0.11		
TK0121	Proline dehydrogenase, delta subunit (2Fe-2S	-0.71	-0.38	-0.55	0.24	-0.95	-0.66	-0.81	0.21		
TK0122	Proline dehydrogenase, beta subunit (dye-linke	-0.11	-0.13	-0.12	0.01	-	-1.54	-	-	coding	
TK0123	Multidrug-efflux transporter_COG0477	0.64	-0.11	0.27	0.53	-	-	-	-	coding	
TK0124	Hypothetical protein	-0.50	-0.61	-0.55	0.08	-0.66	-0.70	-0.68	0.03		
TK0125	N-Acetyltransferase, GNAT family_COG0454	0.37	0.20	0.29	0.12	-0.38	-1.52	-0.95	0.81		
TK0126	Predicted transcription regulator, containing DI	0.50	0.24	0.37	0.18	-0.77	-0.88	-0.82	0.08		5' (+1)
TK0127	Hypothetical protein	-0.65	-0.32	-0.48	0.24	2.58	1.63	2.11	0.67		
TK0128	Predicted nucleic acid-binding protein, containi	-0.86	-0.50	-0.68	0.26	-	0.30	-	-		
TK0129	Hypothetical protein, conserved, DUF356 famil	-1.08	-0.58	-0.83	0.36	-	-0.92	-	-		
TK0130	Hypothetical protein, conserved, DUF114 famil	-0.23	-0.47	-0.35	0.17	-0.37	-0.72	-0.55	0.25		
TK0131	Hypothetical protein, conserved, DUF505 famil	-0.46	-0.53	-0.49	0.05	-	-0.13	-	-	coding	
TK0132	TATA box-binding protein (transcription initiati	0.21	0.00	0.10	0.15	1.59	0.87	1.23	0.51		
TK0133	Hypothetical protein, conserved	0.17	0.14	0.15	0.02	-0.02	1.31	0.64	0.94		
TK0134	Probable acetylpolyamine aminohydrolase, hist	0.01	-0.19	-0.09	0.14	-0.88	0.04	-0.42	0.65		
TK0135	Indolepyruvate: ferredoxin oxidoreductase, beta	-0.27	-0.37	-0.32	0.07	-1.11	-1.01	-1.06	0.07	coding	coding
TK0136	Indolepyruvate: ferredoxin oxidoreductase, alph	-0.07	-0.12	-0.09	0.04	-1.22	-0.99	-1.10	0.16	coding	
TK0137	Predicted nucleic acid-binding protein, containi	-0.23	-0.52	-0.37	0.20	-0.68	-0.73	-0.71	0.04		
TK0138	Hypothetical protein	-0.97	-0.92	-0.94	0.03	-0.63	-0.66	-0.65	0.02		
TK0139	Acetyl-CoA synthetase II (NDP forming), alpha	-0.86	-0.55	-0.71	0.22	-1.62	-0.82	-1.22	0.57	coding	coding
TK0140	Archaeal ATPase, fused to C-terminal DUF234	-1.14	-0.67	-0.90	0.33	-1.03	1.82	0.39	2.02		
TK0141	Hydrolase, metallo-beta-lactamase superfamily	0.04	-0.14	-0.05	0.13	-1.06	-0.92	-0.99	0.09		coding
TK0142	Predicted transcription regulator, containing ce	-0.67	-0.05	-0.36	0.44	0.52	0.38	0.45	0.09		
TK0143	Nucleic acid-binding protein, containing C2H2 z	-0.23	-0.31	-0.27	0.06	-	-	-	-		
TK0144	Hypothetical protein, conserved	-0.60	-0.58	-0.59	0.01	-0.10	-0.34	-0.22	0.17		
TK0145	Hypothetical membrane protein, conserved	-	-0.83	-	-	-0.87	-1.32	-1.09	0.32		
TK0146	Hypothetical membrane protein, conserved	-0.27	-0.31	-0.29	0.03	-	1.54	-	-		
TK0147	Spermidine synthase_COG0421	0.62	0.39	0.50	0.17	-0.51	0.58	0.04	0.77	coding	
TK0148	Hypothetical protein, conserved	-0.51	-0.29	-0.40	0.16	-	1.53	-	-		
TK0149	Pyruvoyl-dependent arginine decarboxylase_CO	0.88	0.58	0.73	0.21	-0.62	-0.46	-0.54	0.11	coding	
TK0150	Glycine cleavage system protein H_COG0509	0.20	-0.04	0.08	0.17	-1.77	-1.21	-1.49	0.39		
TK0151	Transcription regulator, PspC family_COG1983	-0.58	-0.35	-0.47	0.16	-0.14	-0.40	-0.27	0.19		
TK0152	Hypothetical membrane protein, conserved	-0.29	-0.05	-0.17	0.17	-	-	-	-		
TK0153	ATP:dephospho-CoA triphosphoribosyl transfe	0.25	0.12	0.18	0.10	1.34	0.24	0.79	0.78		
TK0154	Hypothetical protein, conserved	-0.46	-0.39	-0.42	0.05	-	-0.87	-	-		
TK0155	RecJ-like exonuclease, containing OB-fold nuc	-0.79	-0.56	-0.67	0.16	0.21	-0.18	0.01	0.28	coding	coding
TK0156	Methyl-accepting chemotaxis protein_COG084	-0.57	-0.79	-0.68	0.15	-	0.37	-	-		
TK0157	Xanthine/uracil permease_COG2252	-1.57	-1.10	-1.34	0.33	-0.54	-1.16	-0.85	0.44	coding	
TK0158	ABC-type iron(III) transport system, ATPase c	-0.67	-0.63	-0.65	0.03	-	1.43	-	-		
TK0159	ABC-type iron(III) transport system, permease	-0.69	-0.51	-0.60	0.13	3.17	-	-	-		coding
TK0160	D-Aminopeptidase_COG3191	0.71	0.34	0.52	0.26	-	-	-	-		
TK0161	ABC-type multidrug transport system, ATPase	2.11	2.49	2.30	0.27	0.19	0.43	0.31	0.17	operon	
TK0162	Hypothetical membrane protein	3.20	3.22	3.21	0.01	0.10	0.24	0.17	0.10	operon	
TK0163	Hypothetical membrane protein, conserved	3.71	3.55	3.63	0.11	-1.24	-0.66	-0.95	0.41	operon	
TK0164	S-layer-like array protein	3.92	3.98	3.95	0.05	0.12	-0.43	-0.15	0.39	operon	
TK0165	Hypothetical protein	4.70	4.46	4.58	0.17	0.61	0.14	0.37	0.33	operon	
TK0166	Hypothetical protein	4.85	4.80	4.83	0.03	-0.05	0.14	0.05	0.13	5' (-28)	
TK0167	Hypothetical protein, conserved, radical SAM s	-0.91	-0.71	-0.81	0.15	-0.06	2.91	1.43	2.10		
TK0168	Predicted transcription regulator, Lrp/AsnC fa	-0.75	-0.39	-0.57	0.25	-0.19	0.14	-0.03	0.23		
TK0169	Predicted transcription regulator, MarR family_	0.18	0.11	0.15	0.05	0.14	0.06	0.10	0.06		
TK0170	Endonuclease IV_COG0648	-0.13	-0.09	-0.11	0.03	0.00	-0.19	-0.09	0.13		
TK0171	Hypothetical protein, conserved	0.52	0.32	0.42	0.14	4.23	0.79	2.51	2.43		
TK0172	Hypothetical membrane protein, conserved, DU	-0.25	0.19	-0.03	0.32	0.06	4.47	2.26	3.12		
TK0173	Hypothetical protein, conserved, DUF77 family	0.37	0.35	0.36	0.01	-0.42	-1.43	-0.92	0.71		
TK0174	Hypothetical protein, conserved, AMMECR1 fa	-0.09	-0.31	-0.20	0.16	-	-0.24	-	-		
TK0175	Hypothetical protein, conserved, DUF207 famil	-0.03	-	-	-	-	-0.85	-	-		
TK0176	Predicted nucleic acid-binding protein, containi	0.70	0.37	0.53	0.23	-	0.04	-	-		

TK0177	Hypothetical protein, conserved	-0.37	-0.21	-0.29	0.12	-	4.23	-	-		
TK0178	DNA helicase, UvrD/REP family_COG1112	-0.39	-0.19	-0.29	0.14	-	0.65	-	-		coding
TK0179	Hypothetical protein, conserved, DUF35 family	-0.17	-0.26	-0.21	0.06	-1.44	-1.88	-1.66	0.31	coding	
TK0180	Acetyl-CoA acetyltransferase_COG0183	-0.32	-0.25	-0.29	0.05	-1.70	-1.87	-1.79	0.12	coding	
TK0181	3-Hydroxy-3-methylglutaryl-CoA synthase_CO	-0.10	-0.52	-0.31	0.29	-2.03	-1.96	-1.99	0.05	coding	
TK0182	Hypothetical protein, conserved, DUF124 famil	-0.82	-0.68	-0.75	0.10	-0.78	-1.34	-1.06	0.39		
TK0183	snoRNP component, Fibrillarin homolog_COG18	-0.57	-0.81	-0.69	0.17	-0.94	-1.41	-1.17	0.33		
TK0184	snoRNP component, Nop56p/58p homolog_CO	0.28	0.22	0.25	0.05	-0.55	-0.47	-0.51	0.05		
TK0185	Translation initiation factor eIF-2B, delta subu	0.25	0.04	0.14	0.15	-0.54	-0.46	-0.50	0.06		
TK0186	Multiple substrate aminotransferase_COG1167	0.26	0.11	0.18	0.10	0.27	-0.28	0.00	0.39		coding
TK0187	Predicted glutamine amidotransferase, class I_C	-0.38	-0.40	-0.39	0.02	-	-	-	-		
TK0188	Hypothetical protein, conserved, radical SAM s	-	0.08	-	-	-	-	-	-		
TK0189	Predicted stress-inducible protein, OsmC/Ohr	-0.39	-0.17	-0.28	0.16	-2.69	-0.52	-1.61	1.54		
TK0190	GMP synthase, glutamine amidotransferase co	-0.01	-0.20	-0.10	0.13	-0.16	-0.74	-0.45	0.41		
TK0191	Predicted nucleic acid-binding protein, contain	-0.96	-0.90	-0.93	0.04	-0.51	-0.08	-0.29	0.30		
TK0192	Hypothetical protein, conserved, DUF104 famil	-0.36	-0.57	-0.46	0.15	-0.49	-0.87	-0.68	0.27		
TK0193	GMP synthase, PP-loop-ATPase component_C	-0.54	-0.80	-0.67	0.18	-	0.37	-	-		
TK0194	Inosine-5'-monophosphate dehydrogenase_CO	-0.83	-0.86	-0.85	0.02	-0.55	-0.43	-0.49	0.09		
TK0195	Hypothetical membrane protein, conserved, co	0.81	0.54	0.68	0.19	0.26	-0.29	-0.01	0.39		
TK0196	Hypothetical protein, conserved, containing DU	-0.53	-0.48	-0.51	0.03	0.18	1.52	0.85	0.95	coding	
TK0197	Phosphoribosylformylglycinamidine synthase II	-0.76	-0.72	-0.74	0.03	1.26	1.06	1.16	0.15		coding
TK0198	Predicted permease, major facilitator superfam	-	-0.11	-	-	-	-1.23	-	-		
TK0199	Predicted permease, major facilitator superfam	-	0.38	-	-	-	-0.90	-	-	coding	
TK0200	Phosphoenolpyruvate synthetase-related prote	1.77	1.78	1.78	0.01	-0.09	0.24	0.07	0.24		
TK0201	Phosphoribosylformylglycinamidine synthase I_C	-	-0.60	-	-	-1.38	-1.55	-1.46	0.12		
TK0202	Phosphoribosylformylglycinamidine synthase, P	-0.55	-0.28	-0.41	0.19	-	2.34	-	-		
TK0203	Hypothetical protein, conserved, containing DU	-0.66	-0.57	-0.61	0.06	0.73	-	-	-		
TK0204	Phosphoribosylamine-glycine ligase_COG0151	-0.58	-0.63	-0.60	0.03	-	0.33	-	-		
TK0205	Hypothetical protein, conserved	0.36	0.28	0.32	0.05	-0.04	-0.17	-0.11	0.09		
TK0206	Hypothetical protein, conserved	0.07	0.08	0.07	0.01	-	-0.98	-	-		
TK0207	Formate-dependent phosphoribosylglycinamide	-0.36	-0.27	-0.31	0.07	0.49	-0.33	0.08	0.58		
TK0208	Phosphoribosylformylglycinamidine cyclo-ligase	-0.44	-0.42	-0.43	0.02	-	0.43	-	-		
TK0209	Hypothetical protein	-0.39	-0.24	-0.32	0.10	-	4.32	-	-		
TK0210	Phosphoribosylaminoimidazole-succinocarboxa	-0.32	-0.17	-0.24	0.10	0.35	-0.20	0.08	0.39		
TK0211	Amidophosphoribosyltransferase_COG0034	-0.58	-0.76	-0.67	0.12	-	-0.55	-	-		
TK0212	Predicted nucleic acid-binding protein, contain	-1.14	-0.85	-0.99	0.20	-	-1.17	-	-		
TK0213	Hypothetical protein, conserved, UPF0175 fami	-0.07	-0.38	-0.22	0.22	-	4.12	-	-		
TK0214	Probable formate dehydrogenase, alpha subuni	0.55	-0.18	0.18	0.52	-	-	-	-	coding	
TK0215	Hypothetical protein, conserved	0.17	0.42	0.29	0.18	0.48	0.28	0.38	0.14	5' (-59)	5' (+41)
TK0216	Pyridoxine biosynthesis amidotransferase, SNO	-0.18	-0.26	-0.22	0.05	-	-	-	-		
TK0217	Pyridoxine/pyridoxal 5-phosphate biosynthesis	-0.09	-0.40	-0.24	0.22	-	-1.49	-	-		coding
TK0218	Nicotinate-nucleotide pyrophosphorylase_COG	-1.03	-0.32	-0.67	0.50	-1.35	-1.22	-1.29	0.09		
TK0219	Sugar-phosphate nucleotidyltransferase_COG1	0.31	0.12	0.21	0.13	1.49	-	-	-		
TK0220	Hypothetical membrane protein	-0.28	-0.16	-0.22	0.09	-0.79	1.56	0.38	1.66		
TK0221	Hypothetical protein, conserved, DUF712 famil	-0.85	-0.43	-0.64	0.30	-0.37	0.90	0.27	0.90		
TK0222	Nucleotidyltransferase_COG1708	-0.38	-0.24	-0.31	0.10	-	3.35	-	-		
TK0223	Predicted permease, major facilitator superfam	0.50	0.76	0.63	0.18	0.89	2.33	1.61	1.02		
TK0224	SAM-dependent methyltransferase, UbiE/COQ	2.01	1.23	1.62	0.56	-	0.88	-	-	coding	
TK0225	Predicted transcription regulator, ArsR family	0.10	0.26	0.18	0.11	-0.28	-0.24	-0.26	0.03		
TK0226	Hypothetical protein, conserved	0.58	0.43	0.50	0.10	3.77	0.39	2.08	2.39		
TK0227	Hypothetical protein, conserved	0.77	0.23	0.50	0.38	-	1.52	-	-		
TK0228	Met-10+ like protein (C-terminus)	-0.47	-0.39	-0.43	0.06	-0.66	-0.17	-0.42	0.34		coding
TK0229	Hypothetical protein	0.07	0.11	0.09	0.03	-	-	-	-		
TK0230	ABC-type multidrug transport system, ATPase	0.92	0.94	0.93	0.01	0.44	0.98	0.71	0.38		
TK0231	ABC-type multidrug transport system, permeas	0.48	0.42	0.45	0.05	-	1.49	-	-		
TK0232	N-Acetyltransferase, GNAT family_COG0454	0.77	1.02	0.90	0.18	-	-	-	-	coding	
TK0233	Ribosomal protein-serine acetyltransferase Rin	2.12	2.14	2.13	0.01	-0.15	0.90	0.37	0.75		
TK0234	Predicted SAM-dependent methyltransferase	1.50	1.46	1.48	0.02	-	2.30	-	-		
TK0235	Predicted permease, major facilitator superfam	0.96	0.60	0.78	0.26	-	-	-	-		
TK0236	Hypothetical protein	0.99	1.33	1.16	0.24	-	-	-	-		
TK0237	Hypothetical membrane protein	0.80	1.27	1.03	0.34	2.72	2.52	2.62	0.14	5' (+34)	
TK0238	Carbon-nitrogen hydrolase_COG0388	1.07	1.15	1.11	0.06	-0.32	-0.85	-0.59	0.38		
TK0239	Putative tRNA-binding protein_COG0073	-0.11	0.29	0.09	0.28	-	1.27	-	-		
TK0240	Arginase_COG0010	-0.24	-0.03	-0.13	0.15	1.64	1.79	1.71	0.11		
TK0241	Protein-tyrosine phosphatase_COG2453	0.39	0.43	0.41	0.03	-0.24	-0.21	-0.23	0.02		
TK0242	ATP phosphoribosyltransferase, predicted regu	-	-0.16	-	-	-	0.07	-	-		
TK0243	ATP phosphoribosyltransferase_COG0040	0.38	-0.13	0.13	0.36	-	-	-	-		
TK0244	Histidinol dehydrogenase_COG0141	-0.47	-0.56	-0.52	0.06	-0.34	0.88	0.27	0.87		
TK0245	Imidazoleglycerol-phosphate dehydratase_COG	-0.83	-0.99	-0.91	0.11	-0.64	-0.05	-0.35	0.42	coding	
TK0246	Imidazoleglycerol-phosphate synthase, subunit	0.50	0.19	0.35	0.22	2.84	-0.84	1.00	2.61		
TK0247	1-(5-Phosphoribosyl)-5-[(5-phosphoribosylam	-0.12	-0.19	-0.15	0.05	1.69	-0.10	0.79	1.26		
TK0248	Imidazoleglycerol-phosphate synthase, cyclase	0.01	0.05	0.03	0.03	1.74	3.37	2.55	1.16	coding	
TK0249	Bifunctional phosphoribosyl-AMP cyclohydrola	-0.19	-0.37	-0.28	0.13	-0.33	4.45	2.06	3.38		
TK0250	Histidinol-phosphate aminotransferase_COG00	0.13	-0.25	-0.06	0.27	-	1.26	-	-		
TK0251	Predicted hydrolase, HAD superfamily	0.20	-0.11	0.04	0.22	-	-0.31	-	-		
TK0252	Indole-3-glycerol phosphate synthase_COG013	-	0.02	-	-	-	-	-	-		
TK0253	Anthranilate phosphoribosyltransferase_COG05	0.65	-0.27	0.19	0.66	4.83	2.96	3.89	1.32	coding	
TK0254	Anthranilate synthase, component I_COG0147	-	-	-	-	-	-	-	-		
TK0255	Anthranilate synthase, component II_COG0512	-	-0.02	-	-	-	-	-	-	coding	
TK0256	N-(5'-Phosphoribosyl)anthranilate isomerase_C	-0.29	-0.19	-0.24	0.07	1.27	-0.57	0.35	1.30		
TK0257	Tryptophan synthase, beta subunit_COG0133	-0.80	-0.63	-0.71	0.13	0.42	0.97	0.70	0.39	coding	
TK0258	Tryptophan synthase, alpha subunit_COG0159	-0.06	-0.23	-0.14	0.12	0.35	0.19	0.27	0.11		
TK0259	Prephenate dehydrogenase_COG0287	-0.49	-0.33	-0.41	0.11	0.06	-	-	-	coding	
TK0260	Probable aromatic aminotransferase_COG0436	-0.09	-0.43	-0.26	0.24	-	2.03	-	-	coding	
TK0261	Predicted chorismate mutase, N-truncation	-0.55	-0.45	-0.50	0.07	0.20	-1.54	-0.67	1.24		
TK0262	Chorismate synthase_COG0082	-	-0.17	-	-	-	-	-	-		
TK0263	5-Enolpyruvylshikimate-3-phosphate synthase	-0.04	-0.22	-0.13	0.13	0.17	0.86	0.52	0.49		
TK0264	Archaeal shikimate kinase_COG1685	-0.42	-0.55	-0.48	0.09	-	-1.20	-	-	coding	
TK0265	Shikimate 5-dehydrogenase_COG0169	-0.49	-0.70	-0.59	0.15	2.36	-0.20	1.08	1.81	coding	
TK0266	3-Dehydroquinate dehydratase_COG0710	-0.96	-0.87	-0.92	0.06	-	0.86	-	-		
TK0267	3-Dehydroquinate synthetase_COG0337	-1.43	-1.06	-1.25	0.26	-0.01	0.15	0.07	0.12		

TK0268	2-Dehydro-3-deoxyphosphoheptonate aldolase	-0.13	-0.40	-0.27	0.19	-0.69	-1.74	-1.21	0.75		
TK0269	Transketolase, C-terminal section_COG3958	-1.24	-1.11	-1.17	0.09	0.42	5.98	3.20	3.93		
TK0270	Transketolase, N-terminal section_COG3959	-0.43	-0.80	-0.61	0.26	-1.11	-1.02	-1.07	0.06		
TK0271	Hypothetical protein, conserved	-0.91	-0.94	-0.93	0.02	-2.26	-1.07	-1.67	0.84		
TK0272	Pyrroline-5-carboxylate reductase, flame shift	-	-0.73	-	-	-	-	-	-		
TK0273	Pyrroline-5-carboxylate reductase, flame shift	0.25	-0.23	0.01	0.34	1.49	-	-	-		coding
TK0274	N2-Acetyl-lysine deacetylase_COG0624	-0.14	-0.23	-0.19	0.06	-	-	-	-		
TK0275	N2-Acetyl-lysine aminotransferase_COG4992	-0.16	-0.18	-0.17	0.01	-1.05	-0.40	-0.72	0.46	coding	
TK0276	N2-Acetyl-aminoadipate kinase_COG0548	-0.32	-0.26	-0.29	0.04	2.07	-	-	-		
TK0277	N2-Acetyl-aminoadipyl-delta-phosphate reduc	-0.14	-0.12	-0.13	0.01	-0.11	-0.74	-0.42	0.45		
TK0278	RimK-related lysine biosynthesis protein_COG0	-0.14	-0.28	-0.21	0.10	-	-	-	-	coding	
TK0279	Probable lysine biosynthesis protein	-	-0.02	-	-	-	-	-	-		
TK0280	Homoisocitrate dehydrogenase_COG0473	-0.19	-0.19	-0.19	0.01	-	1.14	-	-	coding	
TK0281	Homoaconitase, small subunit_COG0066	-0.52	-0.43	-0.48	0.07	0.67	0.59	0.63	0.06	coding	
TK0282	Homoaconitase, large subunit_COG0065	-0.07	-0.46	-0.26	0.27	-	0.95	-	-	coding	
TK0283	Homocitrate synthase_COG0119	-0.93	-0.37	-0.65	0.40	-0.35	4.12	1.89	3.16		
TK0284	NAD(P)H-flavin oxidoreductase_COG0778	-0.31	-0.28	-0.30	0.02	1.18	-0.11	0.53	0.92		coding
TK0285	Archaeal ATPase, fused to C-terminal DUF234	-0.20	-0.30	-0.25	0.07	-	-	-	-		
TK0286	Archaeal ATPase, fused to C-terminal DUF234	-0.05	-0.17	-0.11	0.08	-	2.96	-	-		
TK0287	Archaeal ATPase, fused to C-terminal DUF234	0.08	-0.08	0.00	0.12	-	-	-	-		
TK0288	Phosphonate matabolism protein PhnP homolo	-0.12	-0.45	-0.29	0.24	-	-	-	-		
TK0289	Pyruvate-formate lyase_COG1882	1.14	0.75	0.94	0.27	-	0.14	-	-		
TK0290	Pyruvate-formate lyase-activating enzyme_CO	-0.16	-0.02	-0.09	0.10	-	-0.91	-	-		
TK0291	Hypothetical protein, conserved	0.34	-0.05	0.14	0.28	-	-0.60	-	-		
TK0292	Hypothetical protein, conserved, DUF82 family	-0.63	-0.54	-0.58	0.06	-0.79	-	-	-		
TK0293	Hypothetical protein, conserved, DUF115 famil	-	-0.49	-	-	-	2.35	-	-		
TK0294	Hypothetical membrane protein	-0.56	-0.39	-0.48	0.12	-	-	-	-		
TK0295	Predicted sodium-dependent transporter	-0.50	-0.59	-0.55	0.06	-	-4.15	-	-		
TK0296	Quinolinate synthetase A_COG0379	-0.26	-0.35	-0.30	0.06	-0.84	-0.92	-0.88	0.06		
TK0297	L-Aspartate oxidase (quinolinate synthetase B	-0.65	-0.23	-0.44	0.30	-0.62	-0.09	-0.35	0.37		
TK0298	Probable transposase_COG0675	2.50	2.57	2.54	0.05	2.74	1.25	2.00	1.06		
TK0299	Hypothetical protein, conserved	0.36	0.20	0.28	0.12	0.23	0.17	0.20	0.04		
TK0300	Hypothetical membrane protein	1.48	1.16	1.32	0.23	0.73	1.91	1.32	0.84		
TK0301	Hypothetical membrane protein	2.12	2.59	2.35	0.33	-	1.73	-	-		
TK0302	RNA 2'-phosphotransferase_COG1859	0.42	-0.01	0.21	0.30	-0.84	-0.76	-0.80	0.06		
TK0303	Membrane-bound metal-dependent hydrolase_	0.11	-0.04	0.04	0.10	-	0.86	-	-		
TK0304	NADH oxidase_COG0446	-0.42	-0.36	-0.39	0.04	-1.38	-1.13	-1.26	0.17		
TK0305	Uridylate kinase_COG0528	-0.26	-0.40	-0.33	0.09	-	-1.66	-	-		
TK0306	DEAD/DEAH box RNA helicase_COG0513	-1.00	-0.62	-0.81	0.27	-0.32	1.12	0.40	1.01		
TK0307	SSU ribosomal protein S10P_COG0051	-0.34	-0.05	-0.20	0.20	-	-1.33	-	-		
TK0308	Translation elongation factor EF-1, alpha subu	0.04	0.16	0.10	0.09	-1.76	-1.68	-1.72	0.06	coding	
TK0309	Translation elongation factor EF-2_COG0480	0.09	0.11	0.10	0.02	-0.91	-1.13	-1.02	0.15	coding	
TK0310	Hypothetical protein, conserved	-1.27	-	-	-	-	-	-	-		
TK0311	Hypothetical protein, conserved	0.09	-0.12	-0.01	0.15	-	-	-	-		
TK0312	Metal-dependent phosphohydrolase, HD superf	0.31	0.09	0.20	0.15	1.41	1.64	1.52	0.16		
TK0313	ArgE/DapE-related deacylase_COG0624	-0.16	-0.20	-0.18	0.02	-	-0.38	-	-	coding	
TK0314	Hydrolase, metallo-beta-lactamase superfamily	-0.94	-0.60	-0.77	0.24	-	3.12	-	-		
TK0315	Hypothetical protein, conserved, DUF504 famil	-1.05	-0.70	-0.88	0.25	2.02	-	-	-		
TK0316	Rubrerythrin-related protein, fused to C-termi	-0.09	-0.30	-0.19	0.15	-	-0.62	-	-		
TK0317	TatD-related deoxyribonuclease_COG0084	-0.01	0.16	0.07	0.12	-	1.24	-	-		
TK0318	Hypothetical protein, conserved	0.05	-0.09	-0.02	0.10	2.68	-0.73	0.97	2.41		
TK0319	Pterin-binding protein_COG0294	-0.55	-0.45	-0.50	0.07	-	-	-	-		
TK0320	Hypothetical protein, conserved, DUF72 family	-0.02	0.22	0.10	0.17	-	-	-	-		
TK0321	Hypothetical protein	4.01	3.75	3.88	0.18	-0.18	2.14	0.98	1.64	5' (+8)	5' (-99)
TK0322	Hypothetical membrane protein, conserved	2.56	2.51	2.53	0.04	3.70	0.53	2.12	2.24		
TK0323	Hypothetical membrane protein, conserved	1.97	2.00	1.98	0.02	1.76	0.44	1.10	0.93		
TK0324	Hypothetical membrane protein, conserved	1.30	2.02	1.66	0.51	-0.06	2.90	1.42	2.09		
TK0325	Hypothetical membrane protein, conserved	2.31	2.71	2.51	0.29	2.09	-	-	-		
TK0326	ABC-type multidrug transport system, ATPase	1.70	1.95	1.83	0.17	-	-0.15	-	-		
TK0327	Phosphohydrolase, PHP family_COG1387	-0.13	0.14	0.01	0.19	0.12	1.19	0.65	0.75		
TK0328	Methylmalonyl-CoA mutase, C-terminus of larg	0.66	0.49	0.58	0.12	-1.05	-0.10	-0.57	0.67		
TK0329	Lysine/arginine/ornithine transport system kin	0.82	0.41	0.62	0.29	0.31	1.51	0.91	0.84	coding	
TK0330	Methylmalonyl-CoA epimerase_COG0346	0.09	0.08	0.08	0.01	-1.65	-0.97	-1.31	0.48	coding	
TK0331	N-Acetyltransferase, GNAT family_COG0454	-0.59	-0.42	-0.50	0.13	2.87	0.05	1.46	1.99		
TK0332	Allophanate hydrolase, subunit 2_COG1984	-0.32	-0.49	-0.41	0.12	-	0.62	-	-		
TK0333	Allophanate hydrolase, subunit 1_COG2049	-0.17	-0.31	-0.24	0.10	-	-0.33	-	-		
TK0334	Predicted nucleic acid-binding protein, containi	-	0.54	-	-	-	-	-	-		
TK0335	Hypothetical protein, conserved, DUF104 famil	0.19	0.03	0.11	0.11	1.26	-0.62	0.32	1.33		
TK0336	Hypothetical protein, conserved, LamB/YcsF fa	-0.17	-0.02	-0.10	0.11	-	-0.06	-	-		coding
TK0337	Predicted nucleic acid-binding protein, containi	-0.49	-0.13	-0.31	0.26	-	-	-	-		
TK0338	Predicted nucleotide kinase, related to CMP ar	0.24	0.11	0.17	0.09	0.96	-0.66	0.15	1.14		
TK0339	Hypothetical protein, conserved, containing leu	-0.33	-0.44	-0.38	0.08	-	-1.41	-	-		
TK0340	Hypothetical protein, conserved, DUF103 famil	-0.44	-0.44	-0.44	0.00	5.55	1.15	3.35	3.11		
TK0341	Nucleotidyltransferase, fused to N-terminal DN	-0.40	-0.48	-0.44	0.05	-0.67	0.78	0.06	1.03		
TK0342	Hypothetical protein, conserved	-	0.18	-	-	-	-	-	-		
TK0343	Predicted nucleic acid-binding protein, containi	-	0.06	-	-	-	-0.77	-	-		
TK0344	Hypothetical protein	0.22	0.01	0.11	0.14	1.92	1.12	1.52	0.56		
TK0345	3-Methyladenine DNA glycosylase_COG0122	0.22	0.14	0.18	0.06	-1.16	-0.16	-0.66	0.71		
TK0346	Hypothetical protein, conserved	-0.17	-0.26	-0.21	0.07	1.28	-	-	-		
TK0347	Predicted membrane-bound serine protease, N	0.38	0.21	0.29	0.12	-	-1.52	-	-	coding	coding
TK0348	Predicted membrane protease subunit, stomati	0.24	0.60	0.42	0.25	-1.35	-0.08	-0.71	0.90		
TK0349	ATPase involved in chromosome partitioning, P	0.68	0.67	0.67	0.01	-1.02	-0.77	-0.89	0.18		
TK0350	Hypothetical protein, conserved	0.35	0.53	0.44	0.12	-0.17	1.75	0.79	1.36		
TK0351	Hypothetical protein, conserved	-0.15	0.09	-0.03	0.17	0.80	-0.04	0.38	0.59		
TK0352	Thymidine phosphorylase_COG0213	-0.29	-0.19	-0.24	0.07	-0.37	-0.54	-0.45	0.12		
TK0353	Hypothetical protein	-0.20	-0.23	-0.21	0.02	-0.38	0.16	-0.11	0.38		
TK0354	Molybdenum cofactor biosynthesis protein C_C	0.45	0.59	0.52	0.09	-0.61	-	-	-		
TK0355	ABC-type multidrug transport system, ATPase	0.64	1.08	0.86	0.31	-	1.84	-	-	coding	
TK0356	Hypothetical membrane protein, conserved_CO	0.48	0.82	0.65	0.24	-	-	-	-	coding	
TK0357	Hypothetical membrane protein, conserved_CO	0.36	0.60	0.48	0.17	-0.51	0.32	-0.10	0.59		
TK0358	RNA terminal phosphate cyclase operon orfB h	-0.54	-	-	-	-2.03	-1.67	-1.85	0.26		

TK0359	Hypothetical protein, conserved_COG3270	-0.41	-0.37	-0.39	0.03	0.27	-0.85	-0.29	0.79		
TK0360	tRNA/rRNA cytosine-C5-methylase, NOL1/NO	-0.14	-0.24	-0.19	0.07	-0.86	-0.59	-0.73	0.19	coding	
TK0361	Hypothetical protein, conserved, DUF101 famil	-0.32	-0.33	-0.32	0.01	-0.29	-0.04	-0.17	0.18		
TK0362	Hypothetical protein	0.18	-0.10	0.04	0.20	-	3.06	-	-		
TK0363	3-Methyl-2-oxobutanoate hydroxymethyltrans	0.12	-0.24	-0.06	0.25	-0.14	-	-	-		
TK0364	Dolichol-phosphate mannosyltransferase_COG	-0.72	-0.63	-0.68	0.06	0.47	0.50	0.49	0.02		
TK0365	Membrane-bound phosphoesterase, PAP2 supe	1.27	1.23	1.25	0.03	0.40	1.56	0.98	0.82	5' (-91)	
TK0366	ThiI-related protein_COG0301	-0.54	-0.41	-0.47	0.09	-0.22	-0.35	-0.28	0.09		
TK0367	Hypothetical membrane protein, conserved, DU	-0.20	0.02	-0.09	0.16	-	-	-	-		
TK0368	Thiamine biosynthesis protein ThiI_COG0301	0.12	-0.02	0.05	0.10	-	-1.03	-	-	coding	
TK0369	Hypothetical membrane protein	-0.14	-0.18	-0.16	0.03	-0.28	-0.25	-0.27	0.02		
TK0370	NAD(P)H-flavin oxidoreductase_COG0778	-0.47	-0.31	-0.39	0.11	0.33	-0.39	-0.03	0.51		
TK0371	Hypothetical protein	-0.73	-0.14	-0.44	0.42	-	0.54	-	-	5' (+50)	
TK0372	Hypothetical protein	0.30	0.14	0.22	0.12	1.38	-0.65	0.37	1.44		
TK0373	Hypothetical protein, conserved	-0.25	-0.01	-0.13	0.17	-	1.40	-	-		
TK0374	Predicted nucleic acid-binding protein, contain	-0.63	-0.49	-0.56	0.10	-0.49	-	-	-		
TK0375	Probable maleate cis-trans isomerase_COG347	-0.08	0.04	-0.02	0.09	-1.71	-	-	-		
TK0376	ADP-dependent phosphofructokinase_COG480	-0.33	-0.29	-0.31	0.03	0.15	1.26	0.70	0.78		
TK0377	Hypothetical protein, conserved, DUF835 famil	-0.48	-0.27	-0.37	0.15	-0.35	-0.67	-0.51	0.23		
TK0378	Chromosome partitioning protein ParB homolog	-0.22	-0.13	-0.18	0.06	-	-0.45	-	-		
TK0379	Hypothetical protein, conserved, DUF763 famil	-	-0.66	-	-	-	-	-	-	coding	
TK0380	Hypothetical protein, conserved, DUF89 family	-0.90	-0.33	-0.62	0.40	-	-	-	-		
TK0381	SSV1 integrase homolog, C-fragment_COG434	-	-0.17	-	-	-	-	-	-		
TK0382	Hypothetical protein	-	-0.18	-	-	-	-3.88	-	-		
TK0383	Hypothetical protein	-0.45	-0.59	-0.52	0.10	-	-	-	-		
TK0384	Hypothetical membrane protein, conserved	-0.25	-0.57	-0.41	0.23	-	0.76	-	-		
TK0385	Hypothetical protein, conserved	0.15	0.01	0.08	0.10	-	4.61	-	-	coding	
TK0386	Hypothetical membrane protein, conserved	0.01	-0.25	-0.12	0.19	0.82	1.15	0.99	0.23	coding	
TK0387	Hypothetical membrane protein, conserved	-0.76	-0.56	-0.66	0.14	2.50	4.46	3.48	1.39		
TK0388	Hypothetical membrane protein, conserved	-0.13	-0.23	-0.18	0.07	-	2.63	-	-		
TK0389	Hypothetical membrane protein, conserved	-0.57	-0.42	-0.49	0.10	-	-	-	-		
TK0390	Hypothetical protein, conserved	-0.73	-0.50	-0.62	0.16	1.25	1.11	1.18	0.10		
TK0391	Hypothetical protein, conserved, containing leu	-0.49	-0.34	-0.42	0.10	-	-	-	-		
TK0392	Hypothetical protein, conserved	-	-0.83	-	-	-	-0.91	-	-		
TK0393	Hypothetical membrane protein, conserved, co	-	-0.31	-	-	-	-	-	-		
TK0394	Predicted ATPase, AAA superfamily	-	-0.33	-	-	-	-	-	-		
TK0395	Hypothetical protein, conserved	-0.22	0.17	-0.02	0.28	-	-	-	-		
TK0396	Hypothetical protein	0.27	0.06	0.16	0.15	-	0.23	-	-		
TK0397	Hypothetical membrane protein, conserved	0.96	0.81	0.89	0.10	-	-0.16	-	-	5' (-72)	
TK0398	Hypothetical protein	1.28	1.12	1.20	0.11	-1.41	-1.03	-1.22	0.27	5' (-15)	
TK0399	Hypothetical protien	-0.50	-0.35	-0.42	0.11	-1.04	-1.64	-1.34	0.43		
TK0400	Hypothetical protein	-0.04	0.04	0.00	0.06	-	-0.66	-	-		
TK0401	Hypothetical protein, conserved	-0.16	-0.22	-0.19	0.05	-	-1.04	-	-		
TK0402	Predicted transcription regulator, SpoVT/AbrB	0.38	0.10	0.24	0.20	-0.78	-0.37	-0.57	0.29		
TK0403	Hypothetical membrane protein, conserved	-0.53	-0.57	-0.55	0.03	2.92	1.29	2.10	1.15		
TK0404	Hypothetical protein, conserved	0.44	0.32	0.38	0.08	3.20	0.18	1.69	2.14	5' (-91)	
TK0405	Predicted transcription regulator, SpoVT/AbrB	-0.09	-0.18	-0.14	0.06	-	-	-	-	5' (-132)	
TK0406	Predicted transcription regulator, SpoVT/AbrB	-1.01	-0.55	-0.78	0.33	-	0.51	-	-	operon	
TK0407	Hypothetical protein	0.05	-0.06	-0.01	0.08	-	3.17	-	-		
TK0408	Hypothetical protein, conserved	-0.09	-0.51	-0.30	0.29	0.03	-0.01	0.01	0.03		
TK0409	Predicted transcription regulator, SpoVT/AbrB	-0.20	0.04	-0.08	0.16	-0.33	1.71	0.69	1.45		
TK0410	Hypothetical protein, conserved	-0.72	-0.46	-0.59	0.18	-	-	-	-		
TK0411	Hypothetical protein, conserved	-0.84	-0.62	-0.73	0.16	-	0.99	-	-		
TK0412	Hypothetical protein	-0.64	-0.28	-0.46	0.26	-	-	-	-		
TK0413	Hypothetical protein	-0.20	-0.25	-0.23	0.04	0.08	-0.72	-0.32	0.57		
TK0414	Hypothetical protein	-0.14	-0.37	-0.26	0.16	-	-	-	-		
TK0415	Hypothetical protein	-	-	-	-	-	-	-	-		
TK0416	Hypothetical protein, conserved	-0.94	-0.59	-0.77	0.25	0.36	-0.41	-0.02	0.54		
TK0417	Hypothetical membrane protein	0.63	0.19	0.41	0.31	3.37	3.13	3.25	0.17		
TK0418	Hypothetical protein	-	0.03	-	-	-	0.71	-	-		
TK0419	Hypothetical protein	-0.14	-0.12	-0.13	0.02	0.88	0.20	0.54	0.48		
TK0420	Hypothetical protein, conserved	-0.56	-0.36	-0.46	0.14	-	-1.24	-	-		
TK0421	Predicted integrase, N-fragment	0.09	-0.25	-0.08	0.24	-0.28	0.72	0.22	0.71		
TK0422	tRNA m1G methyltransferase_COG2419	-0.53	0.05	-0.24	0.41	-	-	-	-	coding	coding
TK0423	Prolyl endopeptidase_COG1505	0.39	0.40	0.39	0.01	-0.83	-1.18	-1.01	0.25		
TK0424	Riboflavin biosynthesis protein RibD (Diaminoh	0.29	-0.04	0.12	0.23	0.72	0.91	0.82	0.14		
TK0425	Riboflavin synthase, alpha subunit_COG0307	0.85	0.28	0.57	0.41	-	-0.31	-	-	coding	
TK0426	Hypothetical protein	1.58	1.47	1.52	0.07	-1.37	-1.25	-1.31	0.08		
TK0427	Hypothetical protein	0.56	0.66	0.61	0.07	-0.60	-1.13	-0.87	0.38		
TK0428	Riboflavin biosynthesis protein RibA (GTP cycl	0.21	0.21	0.21	0.00	-	-	-	-		
TK0429	Riboflavin synthase, beta subunit_COG0054	0.33	0.01	0.17	0.23	-1.12	-0.80	-0.96	0.23		
TK0430	Inosine 5'-monophosphate cyclohydrolase_COG	-0.13	-0.15	-0.14	0.02	2.43	0.41	1.42	1.43		
TK0431	Hypothetical protein, conserved, containing DU	-0.16	-0.15	-0.16	0.01	-	-	-	-		
TK0432	Phosphoribosylaminoimidazolesuccinocarboxam	-0.03	-0.02	-0.03	0.01	1.28	0.88	1.08	0.28		
TK0433	Thiamine biosynthesis protein ThiC_COG0422	0.06	-0.20	-0.07	0.18	-	-	-	-	coding	
TK0434	Thiazole biosynthetic enzyme Thi4_COG1635	-	-0.13	-	-	-	-	-	-		
TK0435	Phosphomethylpyrimidine kinase, fused to C-te	-	-0.81	-	-	-	0.00	-	-		
TK0436	ABC-type transporter, ATPase component, fus	-0.17	-0.03	-0.10	0.10	-	-	-	-	coding	
TK0437	Hypothetical protein	0.37	0.37	0.37	0.00	0.83	0.99	0.91	0.12		
TK0438	Hypothetical protein	0.23	0.26	0.24	0.02	-0.99	-0.24	-0.61	0.53		
TK0439	Membrane-associated metalloprotease, CaaX f	0.17	0.01	0.09	0.11	1.26	2.52	1.89	0.89		
TK0440	Hypothetical protein, conserved	0.31	0.06	0.19	0.18	-	-0.82	-	-		
TK0441	FKBP-type peptidyl-prolyl cis-trans isomerase	0.17	0.14	0.15	0.02	-0.25	-0.23	-0.24	0.02	5' (-115)	coding
TK0442	Hypothetical protein, conserved	5.95	5.46	5.71	0.35	0.34	0.23	0.28	0.08	5' (-54)	
TK0443	Hypothetical membrane protein	4.31	4.82	4.57	0.36	1.02	1.29	1.16	0.19	operon	
TK0444	Cysteinyl-tRNA synthetase_COG0215	2.69	2.65	2.67	0.03	0.40	0.76	0.58	0.26		
TK0445	Hypothetical protein, conserved, DUF196 famil	-	0.54	-	-	-	-	-	-		
TK0446	Hypothetical protein, conserved	0.26	0.48	0.37	0.15	1.08	0.27	0.68	0.58		
TK0447	Hypothetical protein, conserved, RAMP superfa	0.02	0.19	0.10	0.12	2.30	1.01	1.66	0.91		
TK0448	Predicted transcription regulator, containing DI	0.27	0.37	0.32	0.07	-	-0.34	-	-		
TK0449	Metal-dependent phosphohydrolase, HD superf	-0.03	0.22	0.10	0.18	-0.58	-1.04	-0.81	0.32		

TK0450	DEAD/DEAH box helicase_COG1203	0.56	0.80	0.68	0.17	3.66	0.94	2.30	1.92			
TK0451	Hypothetical protein, conserved	-	1.58	-	-	-0.68	-0.44	-0.56	0.17			
TK0452	Hypothetical protein, conserved, RAMP superfa	1.79	1.88	1.84	0.07	1.35	0.05	0.70	0.92			
TK0453	Hypothetical protein, conserved, DUF73 family,	1.87	2.18	2.02	0.22	-	0.60	-	-			
TK0454	Hypothetical protein, conserved	1.71	1.92	1.82	0.15	-0.36	0.21	-0.07	0.40			
TK0455	Hypothetical protein, conserved, DUF48 family	-0.17	-0.10	-0.14	0.05	-	1.45	-	-			
TK0456	Predicted nucleic acid-binding protein, containi	0.11	0.01	0.06	0.07	1.17	-0.53	0.32	1.20			
TK0457	Transcription regulator, SpoVT/AbrB family_CO	0.35	0.21	0.28	0.10	-	3.88	-	-			
TK0458	Predicted exonuclease, RecB family_COG1468	-	0.24	-	-	-	-	-	-			
TK0459	Archaeal ATPase_COG1672	0.83	0.73	0.78	0.07	5.38	-	-	-			
TK0460	DEAD/DEAH box helicase, fused to N-termina	1.59	1.72	1.65	0.09	-	-1.46	-	-	coding	coding	
TK0461	Hypothetical protein, conserved, RAMP superfa	2.63	2.38	2.51	0.18	0.08	-0.25	-0.09	0.23			
TK0462	Hypothetical protein, conserved_COG1857	2.58	2.68	2.63	0.07	-0.50	-0.68	-0.59	0.13			
TK0463	Hypothetical protein, conserved	2.31	2.06	2.19	0.18	-1.08	-0.14	-0.61	0.66			
TK0464	Hypothetical protein, conserved, RAMP superfa	2.88	2.40	2.64	0.34	-0.48	-0.47	-0.48	0.00			
TK0465	Acetyl-CoA synthetase I (NDP forming), beta s	-0.65	-0.08	-0.36	0.41	-1.76	-1.35	-1.56	0.28	coding		
TK0466	Hypothetical protein, conserved_COG5316	0.51	0.07	0.29	0.31	-	-	-	-			
TK0467	Hypothetical protein, conserved	0.76	0.67	0.71	0.07	-	-2.70	-	-	coding		
TK0468	Hypothetical protein, conserved	-0.64	0.03	-0.31	0.48	-0.89	-0.67	-0.78	0.16			
TK0469	Hypothetical protein, conserved, containing SW	0.78	1.24	1.01	0.33	-	-	-	-	coding		
TK0470	Reverse gyrase; intein_COG1110	1.26	0.93	1.10	0.24	1.34	-0.53	0.40	1.32	coding		
TK0471	Probable transcription regulator, DUF118 helix-	-6.35	-5.68	-6.02	0.48	-	-	-	-	coding		
TK0472	Hypothetical protein, conserved	-0.53	0.02	-0.25	0.39	-	2.62	-	-			
TK0473	Hypothetical protein, conserved, UPF0148 fami	0.53	0.47	0.50	0.04	0.16	-0.09	0.03	0.17			
TK0474	Arginase_COG0010	-0.25	-0.43	-0.34	0.13	-0.69	-	-	-			
TK0475	D-Arabino 3-hexulose-6-phosphate formaldeh	-0.09	-0.39	-0.24	0.22	-1.50	-1.35	-1.42	0.10			
TK0476	Hypothetical protein, conserved, containing leu	-0.19	-0.62	-0.41	0.30	-	-0.57	-	-			
TK0477	Hydrolase, HAD superfamily_COG1011	-0.56	-0.39	-0.47	0.11	-0.59	-0.76	-0.67	0.12			
TK0478	Hypothetical protein, conserved	-0.22	-0.30	-0.26	0.06	2.57	0.03	1.30	1.80	coding		
TK0479	Hypothetical protein, conserved	0.21	-0.08	0.06	0.20	-	-	-	-			
TK0480	Metal-dependent phosphohydrolase, HD superf	0.18	0.09	0.14	0.07	0.43	0.47	0.45	0.03			
TK0481	RNA-binding protein, containing KH domain_CO	-0.04	-0.11	-0.08	0.04	-	-	-	-			
TK0482	Hypothetical protein, conserved	0.54	0.40	0.47	0.10	-0.63	-0.90	-0.76	0.19			
TK0483	Hypothetical protein, conserved	0.26	0.28	0.27	0.01	0.57	-0.39	0.09	0.68			
TK0484	Hypothetical protein, conserved	0.42	0.18	0.30	0.16	3.41	-0.31	1.55	2.63			
TK0485	Hypothetical protein, conserved	-	-0.29	-	-	-	-	-	-			
TK0486	Hypothetical protein, conserved	-0.51	-0.80	-0.65	0.21	0.07	0.46	0.27	0.28			
TK0487	Hypothetical protein, conserved	-0.30	-0.45	-0.38	0.10	-0.27	0.26	0.00	0.37			
TK0488	Hypothetical protein, conserved	-0.50	-0.41	-0.45	0.06	2.09	0.01	1.05	1.47			
TK0489	Hypothetical protein, conserved	-0.62	-0.39	-0.51	0.16	-	-	-	-			
TK0490	Hypothetical protein, conserved	-0.09	-0.15	-0.12	0.04	1.95	0.20	1.08	1.23			
TK0491	Hypothetical protein, conserved, containing AT	-0.58	-0.50	-0.54	0.06	-	0.81	-	-			
TK0492	Aspartyl-tRNA synthetase_COG0017	0.05	0.04	0.04	0.00	-1.45	-	-	-			
TK0493	Hypothetical membrane protein, conserved, co	0.31	0.07	0.19	0.17	-0.57	-0.69	-0.63	0.08			
TK0494	Bifunctional carboxypeptidase/aminoacylase_C	0.14	-0.03	0.06	0.12	4.10	-0.18	1.96	3.03			
TK0495	Probable transposase_COG0675	1.84	1.80	1.82	0.03	0.20	-	-	-	5' (-35)		
TK0496	Hypothetical membrane protein	-0.32	0.63	0.16	0.68	-	-	-	-	5' (-83)		
TK0497	Met-10+ like protein_COG2520	-0.53	-0.24	-0.39	0.21	-0.40	0.38	-0.01	0.56			
TK0498	Predicted ATPase, AAA superfamily_COG1373	-0.29	-0.02	-0.16	0.19	0.59	1.74	1.16	0.81			
TK0499	Zinc-dependent protease, TldD/PmbA family_C	-0.55	0.07	-0.24	0.44	-0.16	-0.43	-0.29	0.19			coding
TK0500	Hypothetical protein, conserved_COG5428	-0.09	0.27	0.09	0.25	0.80	-0.43	0.18	0.87			
TK0501	Hypothetical protein, conserved	0.94	0.71	0.82	0.16	-0.90	-1.09	-0.99	0.13			
TK0502	Zinc-dependent protease, TldD/PmbA family_C	1.40	1.08	1.24	0.23	-0.46	-0.81	-0.64	0.25			
TK0503	Hypothetical protein, conserved, cupin superfa	-	-0.50	-	-	-	-	-	-			
TK0504	Aspartate racemase_COG1794	0.21	0.22	0.21	0.00	-0.29	-0.50	-0.39	0.15			
TK0505	Magnesium and cobalt transporter_COG0598	0.08	0.00	0.04	0.06	0.28	-	-	-			
TK0506	Predicted GTPase, containing TGS domain_CO	-0.77	-0.35	-0.56	0.30	-1.31	-0.83	-1.07	0.34			
TK0507	Adenylate cyclase, class 2_COG1437	-0.10	-0.24	-0.17	0.10	-	-1.39	-	-			
TK0508	Predicted transcription regulator, Lrp/AsnC fa	0.48	0.26	0.37	0.16	-0.80	-0.77	-0.78	0.02			
TK0509	3-Octaprenyl-4-hydroxybenzoate decarboxyla	0.49	-0.15	0.17	0.45	-	-	-	-			
TK0510	Hypothetical protein, conserved, DUF147 family	0.37	0.31	0.34	0.04	0.63	-0.42	0.11	0.74			
TK0511	Pyruvate kinase_COG0469	0.36	0.28	0.32	0.06	-	-0.38	-	-	coding		
TK0512	Predicted zinc-dependent protease_COG1913	-0.79	-	-	-	-0.57	-0.30	-0.43	0.19			
TK0513	Hypothetical protein, conserved_COG1689	-0.28	-0.22	-0.25	0.04	-	-1.30	-	-			
TK0514	Chromosome condensation protein CrcB homo	-0.27	-0.05	-0.16	0.16	-	-	-	-			
TK0515	Hypothetical protein, conserved, DUF190 family	-0.58	-0.32	-0.45	0.19	0.64	-0.84	-0.10	1.04			
TK0516	Hypothetical protein	-0.36	-0.35	-0.36	0.01	0.59	0.29	0.44	0.21			
TK0517	Phosphopantothenoylcysteine synthetase/dec	-0.66	-0.44	-0.55	0.16	-0.77	-0.62	-0.70	0.10	coding		
TK0518	Hypothetical protein, conserved_COG4087	-0.34	-0.41	-0.38	0.05	-	-	-	-			
TK0519	Hypothetical protein, conserved, UPF0029 fami	0.32	0.20	0.26	0.09	0.07	-0.50	-0.22	0.41			
TK0520	Hypothetical protein, containing leucine zipper	0.92	1.18	1.05	0.18	1.12	3.02	2.07	1.35			
TK0521	DEAD/DEAH box RNA helicase, fused to C-te	-0.46	-0.32	-0.39	0.10	0.72	0.30	0.51	0.30			
TK0522	Carbohydrate esterase, family 1_COG2819	-	-0.62	-	-	-0.71	-0.59	-0.65	0.09			
TK0523	Rubrerythrin_COG1592	0.03	-0.15	-0.06	0.13	-	-	-	-			
TK0524	Rubredoxin_COG1773	0.13	0.14	0.13	0.01	-	-0.63	-	-			
TK0525	Superoxide reductase_COG2033	0.00	0.04	0.02	0.03	-0.74	-0.63	-0.68	0.08			
TK0526	Hypothetical membrane protein, conserved	0.37	0.55	0.46	0.13	0.23	0.40	0.32	0.12			
TK0527	Hypothetical protein, conserved	-0.62	-0.86	-0.74	0.17	-	-0.98	-	-			
TK0528	Serine hydroxymethyltransferase_COG0112	-0.18	-0.19	-0.18	0.01	-0.73	-0.80	-0.77	0.05	coding		
TK0529	Hypothetical protein, conserved	0.11	-0.18	-0.04	0.20	-	0.49	-	-			
TK0530	Hypothetical protein	0.29	0.09	0.19	0.14	2.82	2.47	2.64	0.25			
TK0531	Hypothetical protein	-0.15	0.01	-0.07	0.11	-	-0.63	-	-			
TK0532	Hypothetical protein	0.32	0.12	0.22	0.14	1.16	2.00	1.58	0.59			
TK0533	Archaeal transcription factor S_COG1594	-0.09	0.06	-0.01	0.11	-	-0.62	-	-			
TK0534	Hypothetical protein, conserved	0.22	0.35	0.28	0.09	-	-	-	-			
TK0535	DNA polymerase sliding clamp (proliferating ce	-0.13	0.23	0.05	0.25	-	-0.94	-	-			
TK0536	Hypothetical protein, conserved_COG1711	-0.71	-0.14	-0.42	0.41	0.66	0.43	0.55	0.16			
TK0537	Peroxiredoxin, AhpC/TSA family_COG0450	-0.20	-0.16	-0.18	0.03	-0.82	-0.90	-0.86	0.06	coding		
TK0538	N-Acetyltransferase, GNAT family_COG1670	-0.31	-0.21	-0.26	0.07	1.45	0.97	1.21	0.34			
TK0539	Predicted transcription regulator, containing DI	-0.09	-0.24	-0.17	0.11	-	0.55	-	-			
TK0540	Metal-dependent phosphohydrolase, HD superf	-0.86	-0.44	-0.65	0.30	-0.53	-0.21	-0.37	0.23			

TK0541	Molybdenum cofactor biosynthesis protein Moe	-0.65	-0.51	-0.58	0.09	-0.41	-1.15	-0.78	0.52		
TK0542	Predicted nucleic acid-binding protein, containi	0.00	-0.46	-0.23	0.33	-	-1.40	-	-		
TK0543	Hypothetical protein	-0.58	-0.34	-0.46	0.17	-0.29	-0.30	-0.30	0.01		
TK0544	Molybdenum cofactor biosynthesis protein B_C	-0.26	-0.12	-0.19	0.10	-0.95	-1.16	-1.05	0.15		
TK0545	S-Adenosylmethionine synthetase_COG1812	0.22	0.14	0.18	0.06	-1.29	-0.62	-0.95	0.47	coding	
TK0546	Hypothetical protein, conserved	0.04	0.01	0.03	0.02	-	-	-	-		
TK0547	Metallophosphoesterase, calcineurin superfamil	0.42	0.47	0.44	0.03	-	-	-	-	coding	
TK0548	Aromatic aminotransferase_COG0436	0.00	-0.15	-0.07	0.11	-1.22	-1.02	-1.12	0.14		
TK0549	Carbamoyl transferase, NodU family_COG2192	0.13	0.04	0.09	0.06	1.70	1.39	1.54	0.22		
TK0550	Prolyl-tRNA synthetase_COG0442	-0.41	-0.13	-0.27	0.20	-1.41	-1.58	-1.49	0.12		
TK0551	D-Isomer specific 2-hydroxyacid dehydrogenas	-0.18	0.01	-0.09	0.14	-0.37	2.91	1.27	2.32		
TK0552	Hypothetical protein	0.44	0.26	0.35	0.12	0.42	-0.58	-0.08	0.71		coding
TK0553	Nucleic acid-binding protein, containing OB-fol	0.30	0.15	0.23	0.10	-0.47	0.03	-0.22	0.35		
TK0554	Hypothetical protein, conserved, DUF358 famil	-0.28	-0.15	-0.21	0.09	-	0.89	-	-		
TK0555	Hypothetical protein	-1.01	-0.56	-0.78	0.32	0.43	0.47	0.45	0.03		
TK0556	Translation initiation factor eIF-2B, beta subun	0.33	0.17	0.25	0.11	0.37	0.03	0.20	0.24		
TK0557	Predicted ATPase, DUF265 family_COG1618	-0.98	-0.56	-0.77	0.30	-	-	-	-		
TK0558	Hypothetical protein, conserved, containing CB	-0.27	-0.30	-0.29	0.02	-0.80	-0.93	-0.87	0.09		
TK0559	Transcription regulator, ArsR family_COG0640	-0.07	-0.23	-0.15	0.11	-0.84	0.05	-0.39	0.63		
TK0560	Archaeal chromatin protein, Alba_COG1581	0.34	0.28	0.31	0.04	-1.18	-0.94	-1.06	0.17		
TK0561	Adenylosuccinate lyase_COG0015	-0.43	-0.42	-0.43	0.01	-1.33	-1.18	-1.26	0.11		
TK0562	Predicted DNA-binding protein, DUF134 family	-0.12	-0.05	-0.09	0.05	-0.24	-0.21	-0.23	0.02		
TK0563	6-Pyruvoyl-tetrahydropterin synthase-related	0.29	-0.02	0.13	0.21	-	-0.10	-	-		
TK0564	Hypothetical protein	0.21	-0.03	0.09	0.17	0.36	-0.27	0.05	0.45		
TK0565	Hypothetical protein, conserved, DUF296 famil	0.17	0.29	0.23	0.09	-	-	-	-		
TK0566	DEAD/DEAH box RNA helicase_COG1202	-0.01	0.13	0.06	0.10	-1.09	-0.05	-0.57	0.74		
TK0567	Transcription regulator, Lrp/AsnC family_COG1	-0.06	-0.14	-0.10	0.05	-	1.31	-	-		
TK0568	Tyrosyl-tRNA synthetase_COG0162	-0.40	-0.18	-0.29	0.16	-	-0.72	-	-		
TK0569	Hypothetical protein, conserved	-0.29	-0.53	-0.41	0.17	-1.09	-1.05	-1.07	0.03		
TK0570	ABC-type iron(III) transport system, periplasmi	-0.22	-0.40	-0.31	0.13	-0.90	-1.06	-0.98	0.11		
TK0571	ABC-type iron(III) transport system, permease	-1.33	-1.10	-1.22	0.16	-0.04	-0.81	-0.43	0.54		
TK0572	ABC-type iron(III) transport system, ATPase c	-0.99	-0.93	-0.96	0.04	-0.85	-1.25	-1.05	0.28		
TK0573	Hypothetical protein, conserved, DUF447 famil	-0.95	-0.77	-0.86	0.13	-	-0.56	-	-		
TK0574	Metallophosphoesterase, calcineurin superfamil	-0.13	-0.35	-0.24	0.15	-1.03	-1.09	-1.06	0.04		
TK0575	Predicted integrase, N-fragment	-2.06	-0.44	-1.25	1.14	0.23	1.17	0.70	0.67		
TK0576	Hypothetical protein, conserved	-0.51	-0.30	-0.41	0.15	-	0.36	-	-		
TK0577	Hypothetical protein	-	-0.14	-	-	-	-	-	-		
TK0578	Hypothetical protein, conserved	-0.41	-0.27	-0.34	0.10	-0.14	0.37	0.12	0.36		
TK0579	Hypothetical protein	-0.58	-0.35	-0.46	0.16	-0.34	0.17	-0.09	0.36		
TK0580	Hypothetical protein	-0.59	-0.51	-0.55	0.06	-	-	-	-	5' (+19)	
TK0581	Hypothetical protein	0.21	0.23	0.22	0.01	-	-	-	-		
TK0582	DNA polymerase sliding clamp (proliferating cel	-0.56	-1.00	-0.78	0.31	-	-	-	-		coding
TK0583	Hypothetical protein	-0.60	-0.34	-0.47	0.18	-	-	-	-		
TK0584	Hypothetical protein	-0.48	-0.56	-0.52	0.06	-	-	-	-		
TK0585	Hypothetical protein	-	0.10	-	-	-	-	-	-		
TK0586	Hypothetical protein	-0.07	-0.53	-0.30	0.32	-	-	-	-	coding	
TK0587	Hypothetical protein	-0.65	-0.31	-0.48	0.24	0.46	0.05	0.25	0.29		
TK0588	Predicted transcription regulator, SpoVT/AbrB	-0.57	-0.79	-0.68	0.15	-	-	-	-		
TK0589	Hypothetical protein	0.37	0.82	0.60	0.32	-	-0.25	-	-		
TK0590	Hypothetical protein	0.98	0.83	0.91	0.10	-	-0.92	-	-		
TK0591	Predicted N-acetyltransferase, GNAT family	-0.04	-0.18	-0.11	0.10	-	-0.93	-	-		
TK0592	Hypothetical protein, conserved	-0.20	0.36	0.08	0.39	-	-	-	-		
TK0593	Hypothetical protein, conserved	-0.52	-0.20	-0.36	0.22	-	1.73	-	-		
TK0594	Hypothetical membrane protein	-1.13	-1.02	-1.08	0.08	-0.26	-0.07	-0.16	0.13		
TK0595	Hypothetical membrane protein	-1.28	-1.03	-1.16	0.17	-	-0.75	-	-	5' (-138)	
TK0596	Hypothetical membrane protein	2.11	1.97	2.04	0.10	1.42	-0.36	0.53	1.26	5' (-30)	
TK0597	Hypothetical protein	0.58	0.23	0.41	0.24	-	1.58	-	-		
TK0598	Hypothetical protein	-0.49	-0.16	-0.32	0.23	-	-	-	-		
TK0599	Hypothetical protein	-0.82	-0.55	-0.68	0.20	0.22	3.66	1.94	2.43		
TK0600	Hypothetical protein, conserved	-0.63	-0.59	-0.61	0.03	-0.39	-0.21	-0.30	0.12		
TK0601	Predicted ATPase, AAA superfamily	-	-0.48	-	-	-	-	-	-		
TK0602	Hypothetical protein, conserved, containing leu	-	-	-	-	-	-	-	-		
TK0603	Hypothetical protein, conserved	0.41	0.30	0.35	0.08	-	-	-	-		
TK0604	Hypothetical protein, conserved, containing leu	0.64	-0.04	0.30	0.48	3.69	1.25	2.47	1.72		
TK0605	Hypothetical protein, conserved	-	-0.66	-	-	-	2.39	-	-	coding	
TK0606	Hypothetical membrane protein, conserved	-0.25	-0.32	-0.29	0.05	-	-	-	-		coding
TK0607	Hypothetical membrane protein, conserved	-0.60	-0.47	-0.54	0.09	1.76	1.48	1.62	0.19		
TK0608	Hypothetical membrane protein, conserved	-0.37	-0.29	-0.33	0.05	0.18	-0.80	-0.31	0.69		
TK0609	Hypothetical membrane protein, conserved	0.08	-0.19	-0.05	0.19	3.03	1.03	2.03	1.42	coding	
TK0610	Hypothetical protein, conserved	0.30	0.13	0.22	0.12	3.13	-	-	-	coding	
TK0611	Hypothetical membrane protein, conserved	-0.62	-0.41	-0.52	0.15	1.00	-0.17	0.42	0.83		
TK0612	Hypothetical protein	-	-0.25	-	-	-	-	-	-		
TK0613	Hypothetical membrane protein	-0.52	-0.27	-0.39	0.18	-	-	-	-		
TK0614	SSV1 integrase homolog, C-fragment_COG434	-0.62	-0.68	-0.65	0.04	-	-0.06	-	-		
TK0615	LSU ribosomal protein L37AE_COG1997	0.32	0.36	0.34	0.03	-	-1.45	-	-		
TK0616	DNA-directed RNA polymerase, subunit P_CO	-0.92	-0.17	-0.55	0.53	-	-	-	-		
TK0617	U3 snoRNP component, archaeal imp4 homolog	-0.16	0.02	-0.07	0.13	-	-0.58	-	-		
TK0618	Multisubunit sodium/hydrogen antiporter, MnhE	-0.41	-0.48	-0.44	0.05	-	-0.31	-	-		
TK0619	Multisubunit sodium/hydrogen antiporter, MnhF	-0.64	-0.43	-0.53	0.15	-	-	-	-		
TK0620	Multisubunit sodium/hydrogen antiporter, MnhG	0.28	0.00	0.14	0.20	1.54	1.19	1.37	0.25		
TK0621	Multisubunit sodium/hydrogen antiporter, predi	0.01	-0.11	-0.05	0.09	-	-	-	-		
TK0622	Multisubunit sodium/hydrogen antiporter, predi	-	0.18	-	-	-	1.48	-	-		
TK0623	Multisubunit sodium/hydrogen antiporter, MnhE	-0.59	-0.50	-0.54	0.07	3.79	0.04	1.92	2.65		
TK0624	Multisubunit sodium/hydrogen antiporter, MnhG	-0.50	-0.20	-0.35	0.21	-	-0.50	-	-		
TK0625	Multisubunit sodium/hydrogen antiporter, MnhD	-	-0.21	-	-	-	-	-	-	coding	
TK0626	Predicted regulator of amino acid metabolism,	0.33	0.20	0.26	0.09	-	-1.46	-	-		
TK0627	NapA-type sodium/hydrogen antiporter_COG04	-0.06	-0.12	-0.09	0.04	-	-	-	-		
TK0628	Hypothetical protein, conserved	0.07	0.02	0.05	0.03	-	-0.72	-	-		
TK0629	Chemotaxis signal transduction protein_COG08	1.51	1.38	1.45	0.09	1.38	2.68	2.03	0.92		
TK0630	Methyl-accepting chemotaxis protein_COG084	1.69	1.70	1.69	0.01	0.50	0.74	0.62	0.16		
TK0631	Chemotaxis protein methyltransferase_COG135	-0.88	-0.99	-0.94	0.07	-1.90	-1.86	-1.88	0.03		

TK0632	Chemotaxis response regulator_COG0784	-0.67	-0.93	-0.80	0.18	-0.41	0.54	0.06	0.67		
TK0633	Chemotaxis protein-glutamate methylesterase,	-0.59	-0.79	-0.69	0.14	-	0.67	-	-		
TK0634	Chemotaxis histidine kinase, flame shift	-0.16	-0.44	-0.30	0.20	-0.46	0.34	-0.06	0.57		
TK0635	Chemotaxis histidine kinase, flame shift	-1.00	-0.85	-0.93	0.11	2.13	1.20	1.67	0.66		coding
TK0636	Chemotaxis protein CheC_COG1776	-1.02	-0.95	-0.98	0.05	-	0.90	-	-		
TK0637	Chemotaxis protein CheC_COG1776	-1.15	-1.06	-1.11	0.06	1.49	-	-	-		
TK0638	Methyl-accepting chemotaxis protein_COG084	-0.58	-0.79	-0.69	0.15	-	0.27	-	-		
TK0639	Chemotaxis protein CheD_COG1871	-0.93	-0.86	-0.89	0.05	-	0.34	-	-		
TK0640	Hypothetical protein, conserved, containing leu	0.13	-0.38	-0.12	0.36	-	-0.86	-	-		
TK0641	Hypothetical protein, conserved, DUF439 famil	-0.80	-0.58	-0.69	0.16	-	2.09	-	-	coding	
TK0642	Hypothetical protein, conserved_COG2892	0.13	-0.22	-0.04	0.25	-	-	-	-		
TK0643	Prefoldin, beta subunit_COG1382	0.16	0.13	0.14	0.02	-0.50	-	-	-		
TK0644	Hypothetical protein, conserved	-0.21	-0.11	-0.16	0.07	-	0.82	-	-		
TK0645	Predicted phosphohydrolase, DHH family_COG	-0.02	0.03	0.00	0.04	-	-	-	-		
TK0646	Hypothetical protein, conserved	0.14	0.41	0.28	0.19	-	-	-	-		
TK0647	Hypothetical protein	4.03	3.86	3.94	0.12	0.65	0.68	0.66	0.02		
TK0648	Hypothetical protein, conserved_COG0457	0.67	0.19	0.43	0.34	-	-	-	-	coding	
TK0649	Putative tRNA-binding protein_COG2517	0.12	-0.02	0.05	0.10	-	0.15	-	-		
TK0650	Rubrerythrin-related protein_COG1633	-0.22	-0.23	-0.22	0.00	1.62	0.16	0.89	1.04		
TK0651	NAD(P)-dependent dyhydrogenase, Gfo/Idh/M	-0.63	-0.50	-0.57	0.09	-	0.14	-	-		
TK0652	Heavy-metal cation transporter, ZIP family_CO	-	0.84	-	-	-	-	-	-		
TK0653	Signal recognition particle GTPase_COG0552	-0.36	-0.36	-0.36	0.00	-	-	-	-		
TK0654	Probable transposase_COG0675	-0.44	-0.18	-0.31	0.18	1.54	1.85	1.70	0.22		
TK0655	Predicted site-specific integrase/resolvase_CO	0.14	0.13	0.13	0.00	-0.92	-0.80	-0.86	0.09		
TK0656	Hypothetical protein, conserved	-0.20	-0.39	-0.29	0.13	-1.56	1.37	-0.10	2.07		
TK0657	ABC-type transport system, probable periplasr	-0.43	-0.52	-0.47	0.06	-1.03	-1.11	-1.07	0.06		coding
TK0658	ABC-type transport system, ATPase compone	-1.06	-0.83	-0.95	0.16	0.71	-0.15	0.28	0.61		
TK0659	ABC-type transport system, permease compor	-0.28	-0.40	-0.34	0.09	0.41	1.02	0.72	0.43	coding	
TK0660	ABC-type transport system, permease compor	-0.31	-0.31	-0.31	0.00	0.17	-0.79	-0.31	0.68	coding	coding
TK0661	ABC-type manganese/zinc transport system, p	0.49	0.63	0.56	0.10	-	-0.57	-	-		
TK0662	Hypothetical protein	4.25	3.80	4.03	0.32	3.42	2.05	2.74	0.97		
TK0663	Hypothetical protein, conserved	-0.02	0.00	-0.01	0.01	-1.12	-1.00	-1.06	0.09		
TK0664	Hypoxanthine/guanine phosphoribosyltransfera	0.42	0.13	0.27	0.20	-	-1.12	-	-		
TK0665	Acetyl-CoA synthetase I (NDP forming), alpha	-0.47	-0.36	-0.41	0.08	-1.21	-1.41	-1.31	0.13		
TK0666	Hypothetical protein, conserved	-1.48	-1.10	-1.29	0.26	-0.13	0.06	-0.04	0.14		
TK0667	Metallophosphoesterase, calcineurin superfami	0.34	0.02	0.18	0.23	1.09	-0.16	0.46	0.88		
TK0668	Hypothetical protein, conserved, containing PR	0.04	0.09	0.06	0.04	-	0.62	-	-		
TK0669	CDC48/VCP homolog, AAA superfamily_COG0	-0.33	-0.23	-0.28	0.07	0.09	-0.51	-0.21	0.42		
TK0670	Hypothetical protein, conserved	0.35	0.29	0.32	0.04	-0.06	-0.01	-0.04	0.03		
TK0671	Deoxyhypusine synthase_COG1899	-0.44	-0.20	-0.32	0.17	0.81	1.64	1.22	0.59		
TK0672	Glutamate synthase beta chain-related oxidore	0.09	-0.12	-0.02	0.15	1.66	-	-	-		
TK0673	Short-chain alcohol dehydrogenase_COG1028	-0.07	-0.21	-0.14	0.10	-	0.85	-	-		
TK0674	Nucleotidyltransferase_COG1708	-0.01	-0.01	-0.01	0.01	-	3.33	-	-		
TK0675	Hypothetical protein, conserved, radical SAM s	0.35	0.39	0.37	0.03	-	-0.79	-	-	5' (-171)	
TK0676	ABC-type multidrug transport system, ATPase	-0.43	-0.06	-0.25	0.26	0.22	0.70	0.46	0.34		
TK0677	Zinc-dependent protease HtpX homolog, M48 f	0.44	0.18	0.31	0.19	-0.18	-0.78	-0.48	0.42	coding	
TK0678	Chaperonin, alpha subunit (thermosome, alpha	0.29	0.05	0.17	0.16	-1.42	-1.56	-1.49	0.10		
TK0679	Serine/threonine protein kinase, RIO1 family_C	-0.05	-0.08	-0.06	0.02	0.26	-0.55	-0.14	0.57		
TK0680	Hypothetical membrane protein	-	-0.59	-	-	-0.69	0.37	-0.16	0.74		
TK0681	Hypothetical protein	-	-0.60	-	-	-	-0.79	-	-		
TK0682	MutS-like DNA mismatch repair ATPase_COG1	-0.61	-0.58	-0.59	0.02	0.32	0.07	0.19	0.17	coding	
TK0683	Glyoxylate reductase_COG1052	-0.31	-0.42	-0.37	0.08	-0.50	-0.72	-0.61	0.16	coding	
TK0684	Aromatic amino acid permease_COG0814	-1.05	-0.92	-0.99	0.09	-1.07	-1.74	-1.40	0.47	coding	
TK0685	NAD-dependent protein deacetylase Sir2p hon	-0.92	-0.43	-0.67	0.34	-	-	-	-		
TK0686	Hydrolase, HAD superfamily_COG1011	-	-0.59	-	-	-	-	-	-		
TK0687	Hypothetical protein, conserved, DUF437 famil	-0.12	-0.10	-0.11	0.01	1.68	-0.16	0.76	1.30		
TK0688	Membrane-associated phosphatase, PAP2 sup	-	-0.33	-	-	-	0.29	-	-		
TK0689	Hypothetical membrane protein, conserved_CO	-0.35	-0.25	-0.30	0.07	-0.54	0.44	-0.05	0.69		
TK0690	Molybdopterin oxidoreductase, molybdopterin-	0.18	0.01	0.09	0.13	-	-0.05	-	-		
TK0691	Hypothetical membrane protein, conserved, co	-0.45	-0.34	-0.39	0.08	0.48	-0.07	0.21	0.39		
TK0692	Predicted permease	-0.48	-0.37	-0.42	0.08	-	4.68	-	-		
TK0693	Hypothetical membrane protein, conserved	-0.28	-0.58	-0.43	0.22	-	0.98	-	-		
TK0694	ABC-type multidrug transport system, ATPase	-0.18	-0.22	-0.20	0.03	0.30	-0.39	-0.05	0.48		
TK0695	Hypothetical protein, conserved_COG3609	-0.47	-0.33	-0.40	0.10	-0.20	0.09	-0.06	0.20		
TK0696	Hypothetical protein, conserved_COG1569	-0.99	-0.45	-0.72	0.38	0.14	3.24	1.69	2.19		
TK0697	Predicted transcription regulator, containing D	-0.30	-0.49	-0.40	0.13	-	-0.29	-	-	coding	
TK0698	Zinc-dependent protease, TldD/PmbA family_C	0.75	0.52	0.64	0.16	-	-0.46	-	-	coding	
TK0699	Zinc-dependent protease, TldD/PmbA family_C	0.74	0.56	0.65	0.12	1.23	1.58	1.41	0.25		
TK0700	Nucleotide pyrophosphohydrolase_COG1694	-0.64	-0.25	-0.45	0.28	-	0.40	-	-		
TK0701	ATPase, ParA/MinD family, containing ferredox	-0.07	-0.04	-0.05	0.02	-1.26	-1.25	-1.25	0.00		
TK0702	ATPase, ParA/MinD family, containing ferredox	0.17	0.09	0.13	0.05	-0.97	-1.29	-1.13	0.23	coding	
TK0703	Hypothetical protein, conserved, radical SAM s	0.22	0.07	0.14	0.11	-0.25	0.14	-0.05	0.28	coding	
TK0704	SAM-dependent methyltransferase, UbiE/COQ	-0.73	-0.38	-0.55	0.24	3.32	1.87	2.60	1.02		
TK0705	NADP-dependent glyceraldehyde-3-phosphate	0.37	0.31	0.34	0.04	-0.52	-0.96	-0.74	0.31	coding	
TK0706	ABC-type iron(III)-siderophore transport syste	0.46	0.38	0.42	0.06	-1.43	-1.36	-1.39	0.05	coding	coding
TK0707	ABC-type iron(III)-siderophore transport syste	0.61	0.49	0.55	0.09	-	-	-	-		
TK0708	ABC-type iron(III)-siderophore transport syste	-0.97	-0.35	-0.66	0.43	-1.85	-1.99	-1.92	0.09		
TK0709	Hypothetical protein	0.91	0.81	0.86	0.07	0.88	-	-	-		
TK0710	Hypothetical protein, conserved, DUF364 famil	0.07	0.25	0.16	0.13	-	-	-	-		
TK0711	Hypothetical protein, conserved, UPF0066 fami	0.48	0.22	0.35	0.18	0.86	0.58	0.72	0.20		
TK0712	Hydrolase, metallo-beta-lactamase superfamily	-	-0.50	-	-	-	-	-	-		
TK0713	Hypothetical membrane protein, conserved	-0.19	-0.05	-0.12	0.10	-0.83	-0.75	-0.79	0.06		
TK0714	Iron(II) transport protein B_COG0370	-0.40	-0.62	-0.51	0.15	-	1.52	-	-		
TK0715	Iron(II) transport protein A_COG1918	-0.68	-0.48	-0.58	0.14	-	2.92	-	-	coding	
TK0716	Iron(II) transport protein A_COG1918	-0.60	-0.48	-0.54	0.08	-	-	-	-		
TK0717	ABC-type molybdate transport system, peripla	0.64	0.34	0.49	0.21	-	-	-	-	coding	
TK0718	ABC-type molybdate transport system, perme	-0.06	0.06	0.00	0.09	-	1.63	-	-	coding	
TK0719	ABC-type molybdate transport system, ATPas	-0.83	-0.39	-0.61	0.31	-	0.29	-	-		
TK0720	Hypothetical protein, conserved	-0.50	-0.43	-0.47	0.05	-0.60	-0.50	-0.55	0.07		
TK0721	Hypothetical protein, conserved_COG4344	0.13	-0.09	0.02	0.15	-	1.94	-	-		
TK0722	Probable protein-S isoprenylcysteine O-methy	-0.45	-0.38	-0.41	0.05	-0.46	0.74	0.14	0.85		

TK0723	Iron-molybdenum cofactor-binding protein	-0.95	-0.33	-0.64	0.44	-	-1.71	-	-		
TK0724	Iron-molybdenum cofactor-binding protein_CO	-0.23	-0.19	-0.21	0.03	-1.13	-1.28	-1.21	0.11	coding	
TK0725	Hypothetical protein, conserved	-0.28	-0.03	-0.16	0.18	-0.02	-0.09	-0.05	0.05		
TK0726	ABC-type multidrug transport system, permea	-0.02	0.01	-0.01	0.02	1.73	-	-	-		
TK0727	ABC-type multidrug transport system, ATPase	-0.28	-0.15	-0.21	0.09	-	-	-	-	coding	
TK0728	Hypothetical membrane protein, conserved	-0.32	-0.39	-0.35	0.05	-0.66	-1.51	-1.08	0.60		
TK0729	SAM-dependent methyltransferase, UbiE/COQ	-0.79	-0.68	-0.73	0.07	-	0.77	-	-		
TK0730	ABC-type transport system involved in Fe-S c	-0.20	-0.26	-0.23	0.04	0.07	0.12	0.09	0.03	coding	
TK0731	ABC-type transport system involved in Fe-S c	-1.00	-0.88	-0.94	0.09	-	0.34	-	-		
TK0732	Iron-molybdenum cofactor-binding protein_CO	0.67	0.09	0.38	0.41	-	-0.26	-	-		
TK0733	Hypothetical protein, conserved, DUF104 famil	-1.03	-0.30	-0.66	0.52	-	1.80	-	-		
TK0734	Predicted nucleic acid-binding protein, contain	-0.61	-0.54	-0.57	0.05	-0.07	0.58	0.25	0.46		
TK0735	Hydrolase, metallo-beta-lactamase superfamily	-0.31	-0.35	-0.33	0.02	-	-0.03	-	-		
TK0736	Short-chain alcohol dehydrogenase_COG1028	-0.35	-0.36	-0.35	0.00	-0.41	-0.94	-0.67	0.37		
TK0737	Hypothetical protein, conserved (C-terminus)	-0.44	-0.43	-0.43	0.01	-	-0.92	-	-		
TK0738	Hypothetical membrane protein, conserved	-0.26	-0.33	-0.30	0.05	2.57	-	-	-		
TK0739	Hypothetical membrane protein, conserved	-0.61	-0.42	-0.52	0.13	-	4.12	-	-		
TK0740	iron-sulfur cluster-binding protein	0.18	-0.56	-0.19	0.52	-	-	-	-		
TK0741	Hypothetical protein, conserved	-1.22	-0.72	-0.97	0.36	2.09	-0.08	1.01	1.53		
TK0742	Hypothetical membrane protein, conserved, DU	-1.21	-0.81	-1.01	0.29	-	2.17	-	-		
TK0743	Hypothetical membrane protein, conserved, DU	-0.27	-0.28	-0.27	0.01	-	-0.28	-	-		
TK0744	Hypothetical protein, conserved	-0.01	-0.07	-0.04	0.04	-	0.87	-	-		
TK0745	ABC-type cobalt transport system, permease	-0.36	-0.41	-0.38	0.03	-0.61	-0.83	-0.72	0.15		
TK0746	ABC-type cobalt transport system, ATPase co	-0.43	-0.38	-0.41	0.03	-	0.33	-	-		
TK0747	Bifunctional biotin-protein ligase/biotin operon	-	-0.36	-	-	0.83	0.68	0.75	0.10		
TK0748	Biotin biosynthesis protein BioY_COG1268	-0.18	-0.28	-0.23	0.07	-	-	-	-		
TK0749	Probable molybdopterin-guanine dinucleotide b	-0.78	-0.22	-0.50	0.39	-	-	-	-		
TK0750	Hypothetical protein, conserved	0.55	0.41	0.48	0.10	-	-0.46	-	-		
TK0751	Hypothetical protein, conserved	1.10	1.40	1.25	0.21	0.61	2.43	1.52	1.29	5' (-30)	
TK0752	Acylamino acid-releasing enzyme (acylaminoac	-0.89	-0.55	-0.72	0.24	-	-0.73	-	-	5' (-138)	
TK0753	Hypothetical membrane protein	1.15	0.95	1.05	0.14	-0.32	1.42	0.55	1.22	5' (-72)	
TK0754	Predicted ATPase, DUF699 family, fused to ac	-0.45	-0.05	-0.25	0.28	-	-0.56	-	-	coding	coding
TK0755	Hypothetical protein, conserved, DUF88 family	0.16	0.33	0.24	0.12	-0.25	-0.78	-0.52	0.38		
TK0756	Hypothetical protein, conserved, DUF88 family	0.08	0.04	0.06	0.03	-	-	-	-		
TK0757	ABC-type thiamine transport system, periplasn	-1.05	-	-	-	1.77	0.01	0.89	1.24		
TK0758	Metal-dependent amidohydrolase_COG0402	-0.15	-0.46	-0.31	0.22	-	0.25	-	-		
TK0759	Asparaginyl-tRNA synthetase_COG0017	-0.22	-0.34	-0.28	0.09	-	-0.15	-	-	coding	
TK0760	Archaeosine tRNA-guanine transglycosylase_C	0.12	-0.08	0.02	0.14	-	0.40	-	-		
TK0761	Sodium/phosphate symporter_COG0306	-0.66	-0.02	-0.34	0.45	-	0.92	-	-		
TK0762	Glycosyltransferase, family 2_COG1215	0.14	0.24	0.19	0.07	-	3.74	-	-		
TK0763	Hypothetical protein, conserved	0.02	-0.18	-0.08	0.14	-	0.88	-	-		
TK0764	Large helicase-related protein; intein_COG120	-0.25	-0.18	-0.21	0.05	0.64	1.20	0.92	0.40	coding	coding
TK0765	Glyceraldehyde-3-phosphate dehydrogenase (I	-1.42	-0.94	-1.18	0.34	-1.51	-1.09	-1.30	0.30		
TK0766	Hypothetical membrane protein	-	-0.39	-	-	-	-0.65	-	-		
TK0767	Hypothetical protein, conserved	-0.23	-0.41	-0.32	0.13	-	-	-	-		
TK0768	Hypothetical protein, conserved, YggU family_C	-0.54	-0.34	-0.44	0.14	-	1.03	-	-		
TK0769	Hypothetical protein, conserved, DUF402 famil	0.40	0.11	0.26	0.21	-	-	-	-		
TK0770	Transcription regulator, PadR-like family	0.06	-0.17	-0.06	0.16	-	-0.44	-	-		
TK0771	Hypothetical protein, conserved (N-terminus)	-0.66	-0.59	-0.62	0.06	-	1.69	-	-	coding	
TK0772	Hypothetical membrane protein, conserved_CO	-0.31	-0.36	-0.33	0.03	-	0.42	-	-		coding
TK0773	Predicted ATP-dependent endonuclease, OLD	2.57	2.70	2.64	0.09	-	0.42	-	-	5' (-51)	coding
TK0774	Predicted permease, auxin efflux carrier family	0.93	0.54	0.74	0.28	-	-0.80	-	-		
TK0775	Deblocking aminopeptidase_COG1363	-0.34	0.06	-0.14	0.28	-	-0.48	-	-		
TK0776	Archaeal ATPase_COG1672	0.19	-0.14	0.03	0.23	-0.03	-1.05	-0.54	0.72		
TK0777	Integrase/recombinase_COG0582	-0.65	-0.46	-0.56	0.13	0.66	-0.09	0.29	0.53		
TK0778	Hypothetical protein, conserved, containing To	-0.18	0.03	-0.07	0.14	-0.59	-1.23	-0.91	0.45		
TK0779	Sugar fermentation stimulation protein_COG14	0.31	-0.10	0.10	0.29	-	-1.18	-	-		
TK0780	Hypothetical protein	-	-0.40	-	-	-	-	-	-	coding	
TK0781	Deblocking aminopeptidase_COG1363	-0.35	-0.34	-0.34	0.01	-0.62	-0.53	-0.57	0.07		
TK0782	Hypothetical protein	-	-0.05	-	-	-	-	-	-		
TK0783	Hypothetical membrane protein, conserved	-0.45	-0.22	-0.33	0.16	1.30	0.64	0.97	0.47		
TK0784	ERCC2/XPD/Rad3-related DNA repair helicas	0.06	0.06	0.06	0.00	-	2.24	-	-		
TK0785	Hypothetical protein	-0.21	-0.25	-0.23	0.02	-	2.24	-	-		
TK0786	Integral membrane protein Rhomboid homolog_	-0.28	-0.36	-0.32	0.06	-0.93	-2.82	-1.88	1.34		
TK0787	Archaeal inositol-1-monophosphatase/fructos	-	-0.56	-	-	-0.80	0.69	-0.06	1.06		
TK0788	Hypothetical membrane protein, conserved, DU	-0.06	-0.18	-0.12	0.08	-	3.10	-	-		
TK0789	Glycerol-1-phosphate dehydrogenase_COG037	0.02	-0.05	-0.01	0.04	-0.23	-0.05	-0.14	0.13		
TK0790	Hypothetical protein, conserved, UPF0179 fami	0.73	0.45	0.59	0.19	-0.34	-0.19	-0.26	0.10		
TK0791	Hypothetical protein, conserved, DUF79 family	-0.08	-0.11	-0.09	0.02	-	0.59	-	-		
TK0792	Hypothetical protein	0.27	0.17	0.22	0.07	-	2.11	-	-		
TK0793	Hypothetical protein, conserved, DUF198 famil	-0.66	-0.14	-0.40	0.37	-1.07	-0.24	-0.66	0.58		
TK0794	Putative 5-methylcytosine restriction system,	0.70	0.52	0.61	0.13	-	0.33	-	-		coding
TK0795	Putative 5-methylcytosine restriction system,	0.34	0.41	0.38	0.05	-	0.45	-	-		
TK0796	DNA-binding protein, containing HTH domain o	-	-0.07	-	-	-	0.86	-	-		
TK0797	Hypothetical protein, conserved, DUF530 famil	-0.13	0.05	-0.04	0.13	-0.54	-0.88	-0.71	0.24		
TK0798	Type II DNA topoisomerase VI, subunit A_COG	-	-	-	-	-	-	-	-		
TK0799	Type II DNA topoisomerase VI, subunit B_COG	-0.27	-0.30	-0.29	0.02	-0.45	-1.06	-0.75	0.43		
TK0800	RNA-binding protein, containing KH domain_CO	0.16	-0.02	0.07	0.13	-	-0.57	-	-		
TK0801	Serine/threonine protein kinase Rio1p homolog	-1.10	-0.14	-0.62	0.68	-	0.33	-	-		
TK0802	Translation initiation factor eIF-1A_COG0361	-0.71	-0.38	-0.55	0.23	0.01	-0.53	-0.26	0.38		
TK0803	ABC-type manganese/zinc transport system, A	-0.72	-0.44	-0.58	0.20	1.81	-	-	-		
TK0804	ABC-type manganese/zinc transport system, I	-0.40	-0.32	-0.36	0.06	0.02	-0.60	-0.29	0.44		
TK0805	Ribonuclease HII_COG0164	-	-0.71	-	-	-	-	-	-		
TK0806	Putative membrane-bound dolichyl-phosphate-	-0.69	-0.53	-0.61	0.11	-	-0.48	-	-		
TK0807	Hypothetical protein, conserved_COG0500	-0.23	-0.01	-0.12	0.16	-1.22	-0.37	-0.80	0.61		
TK0808	Hypothetical protein, conserved	-0.16	-0.18	-0.17	0.02	-	1.04	-	-		
TK0809	Glucosamine--fructose-6-phosphate aminotra	-0.59	-0.46	-0.53	0.10	-	-0.72	-	-		coding
TK0810	Oligosaccharyl transferase, STT3 subunit_COG	-	-0.47	-	-	-	-	-	-		
TK0811	Hypothetical protein, conserved	-0.61	-0.60	-0.60	0.01	-	-1.08	-	-		
TK0812	Adenylate kinase_COG0563	-0.54	-0.63	-0.59	0.07	-	-	-	-		
TK0813	Hypothetical protein, conserved, containing leu	-0.01	0.03	0.01	0.03	-0.15	-0.90	-0.53	0.54		

TK0814	Type A flavoprotein_COG0426	0.31	0.20	0.26	0.08	-0.41	-0.66	-0.53	0.18		
TK0815	Peroxiredoxin, AhpC/TSA family_COG1225	-1.04	-0.50	-0.77	0.38	-	0.05	-	-		
TK0816	2-Oxoacid:ferredoxin oxidoreductase, beta sub	-0.58	-0.27	-0.43	0.22	-	1.59	-	-		
TK0817	2-Oxoacid:ferredoxin oxidoreductase, alpha sul	-0.62	-0.55	-0.59	0.04	1.14	0.98	1.06	0.12	coding	
TK0818	Hypothetical protein	-0.35	-0.43	-0.39	0.06	-	-	-	-		
TK0819	Peptide methionine sulfoxide reductase_COG02	-0.11	-0.34	-0.22	0.17	-	-	-	-		
TK0820	Hypothetical protein	-2.27	-2.21	-2.24	0.04	-	0.30	-	-		
TK0821	Hypothetical membrane protein, conserved	-2.23	-2.45	-2.34	0.15	-2.68	-1.89	-2.29	0.55		
TK0822	Hypothetical membrane protein, conserved, co	-0.48	-0.47	-0.48	0.01	-	2.53	-	-		
TK0823	Hypothetical membrane protein	-	-0.09	-	-	-	-	-	-		
TK0824	Hypothetical protein, conserved_COG1633	-0.67	-0.45	-0.56	0.16	-	-1.13	-	-	coding	
TK0825	Hypothetical protein, conserved	-	-	-	-	-	-	-	-		
TK0826	Hypothetical protein, conserved_COG1633	-0.40	-0.22	-0.31	0.12	-1.07	-1.49	-1.28	0.30		
TK0827	Predicted permease, major facilitator superfam	-0.42	-0.28	-0.35	0.10	0.77	2.49	1.63	1.22		
TK0828	NAD(P)H:rubredoxin oxidoreductase_COG0446	-0.87	-0.53	-0.70	0.25	-	-1.21	-	-		
TK0829	Hypothetical membrane protein, conserved, DU	-0.03	-0.30	-0.16	0.19	-	0.01	-	-		
TK0830	Hypothetical protein, conserved (N-terminus)	0.43	0.23	0.33	0.14	1.28	0.44	0.86	0.59		
TK0831	Peroxiredoxin-related protein (C-terminus)	0.47	0.26	0.36	0.14	0.40	0.22	0.31	0.13		
TK0832	Hypothetical membrane protein, conserved	-0.09	-0.14	-0.12	0.04	3.29	0.59	1.94	1.91		
TK0833	Predicted permease, major facilitator superfam	-0.25	-0.38	-0.32	0.09	-	-	-	-		
TK0834	Transcription regulator, Lrp/AsnC family_COG1	0.23	-0.23	0.00	0.32	-0.17	0.06	-0.05	0.17		
TK0835	Phosphoribosylaminoimidazole carboxylase, AT	-0.65	-0.63	-0.64	0.01	-	0.63	-	-		
TK0836	Phosphoribosylaminoimidazole carboxylase, cat	-0.76	-0.44	-0.60	0.22	1.39	0.71	1.05	0.48	coding	
TK0837	Heavy-metal transporting P-type ATPase_COG	0.26	-0.02	0.12	0.20	-0.87	-	-	-	coding	
TK0838	Thioredoxin	-0.12	-0.15	-0.13	0.02	0.55	0.65	0.60	0.07		
TK0839	NAD(P)H-flavin oxidoreductase_COG0778	-0.29	-0.27	-0.28	0.02	-	3.28	-	-		
TK0840	NAD(P)H-flavin oxidoreductase_COG0778	-1.00	-0.26	-0.63	0.52	-	-0.63	-	-		coding
TK0841	Hypothetical membrane protein, conserved	-	-0.35	-	-	-	-	-	-		
TK0842	Arsenical-resistance membrane protein_COG0	-0.38	-0.36	-0.37	0.01	-0.75	-1.16	-0.95	0.29		
TK0843	Trx-linked arsenate reductase (arsenical pump	-0.61	-0.50	-0.56	0.08	-	-0.79	-	-		
TK0844	Tungsten-containing oxidoreductase_COG2414	-0.32	0.05	-0.14	0.26	0.21	-0.33	-0.06	0.38	coding	
TK0845	Oxidoreductase, aldo/keto reductase family_C	0.09	0.11	0.10	0.01	-	-	-	-		
TK0846	Adenosylcobinamide amidohydrolase_COG1865	-0.85	-0.21	-0.53	0.45	-	-	-	-		
TK0847	Hypothetical protein, containing leucine zipper	-0.24	-0.29	-0.27	0.03	-	-0.33	-	-		
TK0848	Hypothetical protein	-0.91	-0.58	-0.74	0.23	-0.44	-	-	-		
TK0849	Hypothetical protein, conserved	0.85	0.80	0.83	0.04	-	-1.15	-	-		
TK0850	Probable transposase_COG0675	-	0.41	-	-	-	-1.52	-	-		
TK0851	Hypothetical protein, conserved, N-truncation	0.74	0.72	0.73	0.01	-	0.35	-	-		
TK0852	Hypothetical protein, conserved, radical SAM s	0.40	0.30	0.35	0.07	-	0.09	-	-	5' (+46)	
TK0853	NaMN:DMB phosphoribosyltransferase_COG203	0.42	0.24	0.33	0.13	-	-0.79	-	-		
TK0854	Cobyric acid synthase_COG1492	0.18	-0.29	-0.05	0.33	0.94	-0.58	0.18	1.07	5' (+7)	
TK0855	Hypothetical protein, conserved	-0.18	-0.23	-0.20	0.03	-	-	-	-		
TK0856	GTP:adenosylcobinamide-phosphate guanylyltr	-	-0.37	-	-	-	-	-	-		
TK0857	Cobalamin-5-phosphate synthase_COG0368	-1.01	-0.99	-1.00	0.01	0.00	0.55	0.27	0.39		
TK0858	Hypothetical protein, conserved, DUF64 family	0.48	-0.14	0.17	0.44	-	-	-	-		
TK0859	Hypothetical protein, conserved	-0.20	-0.40	-0.30	0.15	0.26	1.06	0.66	0.56		
TK0860	Hypothetical protein	-0.08	-0.37	-0.22	0.21	-	-1.02	-	-		
TK0861	ATP-binding protein_COG2102	-0.41	-0.30	-0.36	0.08	1.06	-0.05	0.51	0.78		
TK0862	Hypothetical protein, conserved	-0.42	-0.28	-0.35	0.09	-	-0.67	-	-		
TK0863	Cobinamide synthase_COG1270	-0.39	-0.36	-0.37	0.02	-1.06	-0.31	-0.69	0.53		
TK0864	Threonine-O-3-phosphate decarboxylase_COG	-0.76	-0.37	-0.56	0.28	-	3.78	-	-		
TK0865	Probable vitamin B12 transport protein precurs	-0.17	-0.30	-0.23	0.09	-1.71	-1.71	-1.71	0.00		
TK0866	2,3-Bisphosphoglycerate-independent phospho	-0.18	-0.27	-0.22	0.06	-0.81	-0.79	-0.80	0.02	coding	
TK0867	Sodium/calcium antiporter_COG0530	0.02	-0.23	-0.11	0.18	-0.55	-0.60	-0.57	0.03		
TK0868	Probable bis(5'-adenosyl)-triphosphatase, HIT	-0.87	-0.48	-0.68	0.28	-1.22	-0.79	-1.00	0.31		
TK0869	Hypothetical protein	-0.88	-0.70	-0.79	0.13	-0.63	-0.83	-0.73	0.14		
TK0870	Alternative thymidylate synthase_COG1351	-0.88	-0.40	-0.64	0.34	-0.13	0.19	0.03	0.22		
TK0871	Ornithine carbamoyltransferase_COG0078	0.21	0.02	0.12	0.14	-0.53	-0.18	-0.35	0.25		
TK0872	tRNA/rRNA cytosine-C5-methylase, NOL1/N	-	0.19	-	-	-	-	-	-		
TK0873	Hypothetical protein, conserved	-0.58	-0.49	-0.54	0.07	-	-	-	-		
TK0874	Predicted metallophosphoesterase, calcineurin	-0.80	-0.78	-0.79	0.01	0.47	3.45	1.96	2.10		
TK0875	Saccharopine reductase_COG1748	-0.87	-0.76	-0.81	0.08	3.29	-	-	-		
TK0876	Ribosome biogenesis protein Nep1p homolog, s	-0.58	-0.77	-0.67	0.14	-	-0.04	-	-		
TK0877	Hypothetical membrane protein, conserved	-1.19	-1.37	-1.28	0.12	0.02	1.20	0.61	0.83		
TK0878	Translation initiation factor eIF-5A_COG0231	-0.62	-0.28	-0.45	0.24	-1.30	-1.21	-1.25	0.07		
TK0879	Hypothetical protein, conserved	-0.59	-0.55	-0.57	0.03	-	0.08	-	-		
TK0880	Arsenical pump membrane protein_COG1055	-	-	-	-	-	-	-	-	coding	
TK0881	Universal stress protein_COG0589	-0.65	-0.54	-0.60	0.08	-	-	-	-		
TK0882	Agmatinase_COG0010	-0.18	0.00	-0.09	0.12	-	1.08	-	-		
TK0883	Hypothetical protein, conserved, containing CB	-1.13	-0.67	-0.90	0.32	-0.03	0.08	0.03	0.08		
TK0884	NapA-type sodium/hydrogen antiporter_COG0	-0.03	-0.19	-0.11	0.11	3.04	0.00	1.52	2.15		
TK0885	Hypothetical protein, conserved	0.06	-0.06	0.00	0.09	1.95	0.61	1.28	0.95		
TK0886	Voltage-gated chloride channel protein_COG00	-1.39	-0.54	-0.96	0.60	0.11	0.49	0.30	0.27		
TK0887	Phosphohydrolase, PHP family_COG1379	-0.79	-0.55	-0.67	0.17	1.44	2.86	2.15	1.01		
TK0888	Transcription regulator, SpoVT/AbrB family	-0.30	-0.16	-0.23	0.10	-	2.06	-	-		
TK0889	Predicted nucleic acid-binding protein, contain	0.52	-0.04	0.24	0.39	-	-0.68	-	-		
TK0890	Thiamine monophosphate kinase_COG0611	-0.03	0.07	0.02	0.07	-	-	-	-		
TK0891	Glycosyltransferase, family 4_COG0438	0.43	0.76	0.59	0.23	-0.85	-0.08	-0.47	0.55		
TK0892	Polysaccharide deacetylase_COG0726	0.84	0.67	0.76	0.12	2.04	-0.46	0.79	1.77		
TK0893	Pyruvate fromate-lyase activating enzyme-rela	0.51	0.34	0.43	0.12	0.16	2.11	1.14	1.38		
TK0894	Hypothetical protein, conserved	0.16	-0.14	0.01	0.22	-0.56	-	-	-		
TK0895	S-layer protein precursor	-1.07	-0.83	-0.95	0.17	-0.89	-1.33	-1.11	0.31	coding	
TK0896	Hypothetical membrane protein, conserved	0.24	0.06	0.15	0.12	-0.44	-0.67	-0.55	0.17		
TK0897	Hypothetical protein, conserved, radical SAM s	-0.03	-0.16	-0.09	0.10	-0.84	-1.50	-1.17	0.47		
TK0898	Hypothetical protein, conserved, C-truncation	0.02	-0.12	-0.05	0.10	-	1.10	-	-		
TK0899	Dimethyladenosine transferase (16S rRNA dim	-0.20	-0.14	-0.17	0.04	0.50	-0.07	0.22	0.41		
TK0900	Hypothetical protein, conserved, DUF655 famil	-0.32	-0.20	-0.26	0.09	-0.91	-0.97	-0.94	0.04		
TK0901	DNA-directed RNA polymerase, subunit F_COG	0.14	0.16	0.15	0.01	-0.60	-0.85	-0.73	0.18		
TK0902	LSU ribosomal protein L21E_COG2139	0.89	0.43	0.66	0.32	-0.75	-0.86	-0.80	0.08		
TK0903	RNA-binding protein, containing THUMP domai	-1.25	-0.29	-0.77	0.68	-0.93	-0.72	-0.82	0.15		
TK0904	Hypothetical protein, conserved_COG3357	-0.51	-0.67	-0.59	0.11	-	-	-	-		

TK0905	Hypothetical membrane protein	-0.21	-0.30	-0.26	0.06	-	-1.05	-	-		
TK0906	Endonuclease V (deoxyinosine 3'-endonuclease	0.39	0.08	0.24	0.22	-	-	-	-		
TK0907	DNA-binding protein Translin homolog_COG217	-0.21	-0.31	-0.26	0.07	-	-0.65	-	-		
TK0908	Archaeal Glu-tRNA(Gln) amidotransferase, sub	-0.53	-0.17	-0.35	0.25	-0.22	-0.19	-0.21	0.02		
TK0909	Hypothetical protein, conserved, DUF104 famil	0.06	0.17	0.12	0.08	-	-	-	-		
TK0910	Predicted nucleic acid-binding protein, contain	-0.29	-0.23	-0.26	0.04	-	1.01	-	-		
TK0911	Archaeal Glu-tRNA(Gln) amidotransferase, sub	-0.37	-0.33	-0.35	0.03	-1.09	-1.69	-1.39	0.42		
TK0912	Hypothetical membrane protein, containing leu	-0.21	-0.27	-0.24	0.05	-	0.10	-	-		
TK0913	Hypothetical protein	1.08	0.94	1.01	0.10	2.89	2.63	2.76	0.19	coding	
TK0914	3-Hydroxy-3-methylglutaryl-CoA reductase_C	-0.08	-0.16	-0.12	0.05	-0.40	-0.55	-0.47	0.11		
TK0915	ATPase involved in chromosome partitioning, P	-0.83	-0.92	-0.87	0.06	-	-0.30	-	-		
TK0916	Threonine 3-dehydrogenase_COG1063	0.21	0.00	0.10	0.15	-0.68	-0.40	-0.54	0.20		
TK0917	Hypothetical protein, conserved, UPF0175 fami	0.04	-0.14	-0.05	0.12	-	-1.18	-	-		
TK0918	Hypothetical protein, conserved_COG2405	0.58	0.13	0.35	0.32	-0.18	0.28	0.05	0.33		
TK0919	Hypothetical protein	0.08	-0.01	0.03	0.06	-	2.09	-	-		
TK0920	Hypothetical protein	-0.59	-0.33	-0.46	0.18	-	-	-	-		
TK0921	Phenylalanyl-tRNA synthetase, alpha subunit_C	-0.13	-0.18	-0.15	0.04	-0.21	-0.57	-0.39	0.26		
TK0922	Hypothetical protein, conserved	0.29	0.24	0.27	0.04	-	-	-	-		
TK0923	Hypothetical protein	0.37	0.09	0.23	0.20	0.65	0.49	0.57	0.12		
TK0924	Predicted nucleic acid-binding protein, contain	-0.25	-0.04	-0.15	0.14	-0.33	-1.07	-0.70	0.52		
TK0925	Phenylalanyl-tRNA synthetase, beta subunit_C	-0.69	-0.30	-0.50	0.28	-	-0.55	-	-		
TK0926	Hypothetical protein	-0.11	-0.20	-0.16	0.06	-	-	-	-		
TK0927	tRNA pseudouridine synthase A_COG0101	-0.22	-0.27	-0.25	0.03	-	1.81	-	-		
TK0928	Predicted DNA/RNA repair helicase_COG1061	0.33	0.35	0.34	0.02	0.88	0.56	0.72	0.23		
TK0929	3-Octaprenyl-4-hydroxybenzoate decarboxyly	-0.57	-0.26	-0.41	0.23	-	-0.11	-	-		
TK0930	Hypothetical protein, conserved	-0.26	-0.04	-0.15	0.15	-	-1.43	-	-		
TK0931	Probable transposase_COG0675	-	-0.05	-	-	-	-0.78	-	-		
TK0932	IS200-like transposase_COG1943	-0.50	-0.29	-0.39	0.15	-0.29	0.07	-0.11	0.26		
TK0933	Hypothetical protein, conserved	0.55	0.34	0.44	0.14	-	-	-	-		
TK0934	Molybdopterin-guanine dinucleotide biosynthes	-0.06	0.16	0.05	0.16	-	-	-	-		
TK0935	TRAP-type transporter, periplasmic componen	-0.24	0.01	-0.11	0.18	-	-0.63	-	-	5' (+32)	
TK0936	Hypothetical protein	-0.64	-0.22	-0.43	0.30	-	-	-	-		
TK0937	TRAP-type transporter, fused permease comp	-0.38	-0.25	-0.32	0.09	-	-	-	-	coding	
TK0938	Hypothetical protein, containing ATP/GTP-bin	0.08	-0.02	0.03	0.07	-	0.97	-	-		
TK0939	GHMP kinase_COG1907	0.24	0.22	0.23	0.02	-	-0.18	-	-		coding
TK0940	Hypothetical protein, conserved_COG4047	0.90	0.05	0.48	0.61	-	-	-	-		
TK0941	Hypothetical membrane protein, conserved_CO	3.72	3.49	3.60	0.16	1.04	0.36	0.70	0.48		
TK0942	ABC-type multidrug transport system, ATPase	4.17	3.57	3.87	0.42	0.74	0.37	0.56	0.26		
TK0943	Acetyl-CoA synthetase II/archaeal succinyl-C	0.56	-0.12	0.22	0.48	-0.19	0.13	-0.03	0.23		
TK0944	Acyl-CoA synthetase (NDP forming), large sub	-0.12	-0.07	-0.09	0.03	-0.20	-0.27	-0.24	0.04	coding	
TK0945	Nucleotidyltransferase_COG2413	-0.49	-0.25	-0.37	0.17	-0.89	-0.76	-0.83	0.09		
TK0946	Hypothetical protein, conserved	0.05	0.11	0.08	0.05	-	-0.76	-	-		
TK0947	Hypothetical protein, conserved_COG0457	0.11	-0.05	0.03	0.12	-	-0.24	-	-		
TK0948	Putative translation factor Sua5p homolog_CO	-0.44	-0.53	-0.49	0.06	-	-	-	-		
TK0949	Glycosyltransferase, family 4_COG0438	-0.03	0.12	0.05	0.11	-	-	-	-		
TK0950	Asparagine synthase (glutamine-hydrolyzing)_C	-0.56	-0.45	-0.51	0.07	0.58	-1.09	-0.26	1.18	coding	
TK0951	XPA-binding protein 1 homolog_COG1100	-0.18	-0.21	-0.20	0.02	-	-0.90	-	-		
TK0952	ATPase involved in chromosome partitioning, P	-0.01	0.06	0.03	0.04	-0.73	-0.43	-0.58	0.21		
TK0953	Predicted ATPase, AAA superfamily, containing	-0.21	-0.09	-0.15	0.09	-0.15	-0.06	-0.10	0.06		coding
TK0954	Septum formation inhibitor Maf homolog_COG0	-0.23	-0.23	-0.23	0.01	0.33	-	-	-	coding	
TK0955	Sugar-phosphate nucleotidyltransferase_COG1	-0.57	-0.54	-0.56	0.02	-0.73	-0.82	-0.77	0.06		
TK0956	LexA-related DNA-binding protein	-0.25	-0.24	-0.24	0.01	-	-	-	-		
TK0957	Iron(II) transport protein B_COG0370	-0.49	-0.26	-0.37	0.16	-	4.27	-	-		
TK0958	Iron(II) transport protein A_COG1918	-0.86	-0.34	-0.60	0.36	-	-	-	-		
TK0959	Hypothetical membrane protein, conserved, UP	-0.13	-0.07	-0.10	0.04	-	-	-	-		
TK0960	Predicted ATPase, PP-loop superfamily_COG0	-0.34	-0.11	-0.23	0.16	-	-0.37	-	-		
TK0961	Hydrogenase expression/formation protein Hyp	0.19	-0.05	0.07	0.17	3.52	0.27	1.90	2.29		
TK0962	Nucleotidyltransferase	0.55	0.40	0.47	0.11	-	0.85	-	-		
TK0963	Hypothetical protein, conserved, DUF712 famil	-0.60	-0.23	-0.42	0.27	-	4.28	-	-		
TK0964	Cell division protein pelota homolog_COG1537	-0.58	-0.48	-0.53	0.07	-	-0.16	-	-		coding
TK0965	Hypothetical protein, conserved, DUF79 family	-0.56	-0.66	-0.61	0.07	-	-	-	-		
TK0966	Hypothetical protein, conserved	-0.87	-0.60	-0.74	0.19	1.26	0.99	1.13	0.19		
TK0967	Xaa-Pro aminopeptidase_COG0006	-0.09	-0.13	-0.11	0.03	-0.83	-0.85	-0.84	0.01	coding	
TK0968	Predicted hydrolase, HAD superfamily_COG101	-0.34	0.04	-0.15	0.27	0.66	1.34	1.00	0.48		
TK0969	LSU ribosomal protein L35AE_COG2451	-0.40	-0.22	-0.31	0.13	-	0.08	-	-		
TK0970	N2,N2-Dimethylguanosine tRNA methyltransfer	-0.62	-	-	-	-1.71	-0.24	-0.97	1.04	coding	coding
TK0971	Hypothetical membrane protein, conserved, DU	-0.07	-0.06	-0.06	0.00	-0.52	0.17	-0.18	0.49		
TK0972	Predicted nucleic acid-binding protein, contain	-0.04	-0.13	-0.08	0.07	0.70	1.27	0.98	0.40		
TK0973	Hypothetical protein, conserved	0.20	0.25	0.23	0.03	-	-	-	-		
TK0974	Sodium-driven multidrug efflux pump protein_C	-0.11	-0.06	-0.09	0.04	-0.25	-1.53	-0.89	0.90		
TK0975	LSU ribosomal protein L37E_COG2126	0.48	0.31	0.39	0.12	-0.75	-1.11	-0.93	0.25		
TK0976	snRNP component, Sm-like protein_COG1958	0.16	0.11	0.14	0.04	-0.74	-1.53	-1.14	0.56		
TK0977	Pullulanase type II, GH13 family_COG0366	-0.66	-0.47	-0.56	0.14	0.35	8.78	4.56	5.96	coding	
TK0978	Glycyl-tRNA synthetase_COG0423	-0.08	0.01	-0.03	0.06	-1.00	-0.78	-0.89	0.15		
TK0979	Hypothetical membrane protein, conserved, DU	-0.14	-0.37	-0.26	0.16	-0.55	-	-	-		
TK0980	Hypothetical membrane protein	-0.23	-0.24	-0.24	0.00	-	-	-	-		
TK0981	N2,N2-Dimethylguanosine tRNA methyltransfer	0.28	0.29	0.28	0.01	-	1.85	-	-	coding	
TK0982	Hypothetical membrane protein	0.77	0.99	0.88	0.16	-0.67	-0.24	-0.46	0.31		
TK0983	Hypothetical protein	0.17	0.04	0.10	0.09	-0.15	-0.16	-0.15	0.00	5' (+4)	
TK0984	Alanyl-tRNA synthetase-related protein (partia	0.36	0.10	0.23	0.18	-	0.99	-	-		
TK0985	Hypothetical protein	-0.80	-0.45	-0.63	0.24	-0.93	-0.69	-0.81	0.17		
TK0986	Proton/glutamate symporter, SDF family_COG1	-	-0.37	-	-	-	-	-	-	coding	
TK0987	Biotin-protein ligase_COG0340	-0.13	-0.15	-0.14	0.01	0.54	1.70	1.12	0.82		
TK0988	Hypothetical protein	-0.33	-0.15	-0.24	0.13	-1.60	-1.01	-1.30	0.42		
TK0989	DhnA-type fructose-1,6-bisphosphate aldolase	-2.00	-0.33	-1.17	1.18	-0.95	-0.31	-0.63	0.45	coding	
TK0990	Oxaloacetate decarboxylase, alpha subunit_CO	-0.18	-0.15	-0.16	0.02	0.03	0.73	0.38	0.49		
TK0991	Carbon starvation protein A_COG1966	-0.62	-0.61	-0.62	0.01	-3.36	-0.48	-1.92	2.04		
TK0992	Hypothetical protein, conserved	-1.00	-0.82	-0.91	0.13	4.52	-	-	-		
TK0993	Hypothetical protein, conserved	0.09	-0.27	-0.09	0.25	0.08	0.73	0.41	0.46		
TK0994	Arsenical pump-driving ATPase_COG0003	-	-0.51	-	-	-	0.42	-	-		
TK0995	Hypothetical protein, conserved, DUF59 family	-0.64	-0.59	-0.62	0.03	-	-0.70	-	-		

TK0996	Hypothetical membrane protein, conserved	-0.67	-0.54	-0.61	0.09	-	1.16	-	-		
TK0997	Transcription regulator, SpoVT/AbrB family_CO	0.07	0.02	0.05	0.03	-	-0.64	-	-		
TK0998	Predicted nucleic acid-binding protein, contain	-0.52	-0.57	-0.55	0.04	1.03	4.54	2.78	2.48		
TK0999	Lysophospholipase, alpha/beta hydrolase super	-0.13	0.11	-0.01	0.17	-	0.81	-	-		
TK1000	Hypothetical membrane protein	-0.65	-0.36	-0.51	0.21	-	-	-	-		
TK1001	Hypothetical protein, conserved	-0.08	-0.10	-0.09	0.01	2.92	-	-	-		
TK1002	Adenylosuccinate synthase_COG0104	-0.45	-0.49	-0.47	0.03	-	-1.31	-	-		
TK1003	Hypothetical protein, conserved	-0.25	-0.05	-0.15	0.14	-0.37	-0.38	-0.37	0.00		
TK1004	UDP-glucose 4-epimerase_COG0451	0.02	-0.12	-0.05	0.10	-0.54	-0.55	-0.55	0.01	coding	
TK1005	Prefoldin, alpha subunit_COG1730	-0.75	-0.13	-0.44	0.44	-0.78	-0.83	-0.80	0.03		
TK1006	Hypothetical protein, conserved	0.65	0.42	0.54	0.16	-1.31	-1.02	-1.17	0.20		
TK1007	Predicted permease, major facilitator superfam	-0.48	-0.36	-0.42	0.08	-0.03	0.45	0.21	0.34		
TK1008	Fe-containing alcohol dehydrogenase_COG145	0.19	0.45	0.32	0.18	-	0.96	-	-		
TK1009	Putative 5-methylcytosine restriction system,	-0.27	0.00	-0.13	0.19	-	-	-	-	coding	
TK1010	Putative 5-methylcytosine restriction system,	-0.05	0.09	0.02	0.10	-	-	-	-		
TK1011	Permease, major facilitator superfamily, flame s	-0.44	-0.38	-0.41	0.04	5.39	-1.29	2.05	4.73		
TK1012	Permease, major facilitator superfamily, flame s	-1.08	-0.44	-0.76	0.45	-0.90	-	-	-		
TK1013	Hypothetical protein, conserved, DUF104 famil	0.07	-0.37	-0.15	0.31	-	0.86	-	-		
TK1014	Predicted nucleic acid-binding protein, contain	0.08	-0.17	-0.05	0.17	-	0.21	-	-		
TK1015	Large helicase-related protein_COG1201	-0.89	-0.38	-0.64	0.36	-	-0.69	-	-		
TK1016	Hypothetical protein, conserved (C-terminus)	0.91	0.81	0.86	0.07	-0.37	-1.06	-0.72	0.49		
TK1017	Chromosome segregation ATPase_COG1196	-0.23	-0.20	-0.22	0.02	-0.74	-2.14	-1.44	0.99		
TK1018	Hypothetical protein, conserved, DUF173 famil	-0.03	-0.01	-0.02	0.01	1.00	-0.30	0.35	0.92		
TK1019	Hypothetical protein, conserved	-	-0.33	-	-	-	-	-	-		
TK1020	Hypothetical membrane protein	-0.51	-0.45	-0.48	0.04	0.02	-0.15	-0.07	0.13		
TK1021	Helicase-associated endonuclease for fork-str	-0.20	-0.44	-0.32	0.17	0.61	-0.89	-0.14	1.06		coding
TK1022	D-Aminopeptidase_COG2362	0.35	0.68	0.51	0.24	0.31	-0.59	-0.14	0.63		
TK1023	Hypothetical protein, conserved	-0.14	-0.02	-0.08	0.08	1.62	-0.39	0.62	1.42		
TK1024	Hypothetical membrane protein	5.23	4.76	4.99	0.33	0.04	0.17	0.10	0.10	operon	
TK1025	Hypothetical protein, conserved, containing AT	4.88	4.59	4.73	0.21	0.23	0.11	0.17	0.08	5' (-163)	
TK1026	Geranylgeranylglyceryl diphosphate synthase_C	0.49	0.12	0.30	0.26	-	-0.95	-	-		
TK1027	Predicted nucleic acid-binding protein, contain	-	-0.38	-	-	-	-	-	-		
TK1028	Hypothetical protein, conserved, DUF104 famil	-	-0.53	-	-	-	-	-	-		
TK1029	Hypothetical protein, conserved, DUF123 famil	-0.35	-0.52	-0.43	0.12	-	-	-	-		
TK1030	Hypothetical protein, conserved_COG4003	0.02	-0.20	-0.09	0.15	-0.64	-0.93	-0.79	0.20		coding
TK1031	Predicted ATPase, RNase L inhibitor homolog_	-0.88	-0.49	-0.68	0.28	-0.81	-0.42	-0.62	0.28		
TK1032	Hydrogenase expression/formation protein Hyp	-0.51	-0.29	-0.40	0.15	-	-	-	-		coding
TK1033	Predicted metalloprotease, containing Jab1/MI	0.26	-0.05	0.11	0.22	-	-	-	-		
TK1034	Predicted restriction endonuclease_COG2810	-	-	-	-	-	-	-	-		
TK1035	Predicted glutamine amidotransferase, class II_	-0.41	-0.25	-0.33	0.11	-0.48	0.23	-0.13	0.50		
TK1036	Hypothetical protein, conserved, containing CB	0.67	-0.29	0.19	0.68	0.69	1.62	1.15	0.66		
TK1037	Metallophosphoesterase, calcineurin superfami	-0.37	-0.29	-0.33	0.05	-0.89	-1.64	-1.26	0.53		coding
TK1038	2-Phosphoglycerate kinase_COG2074	-0.54	-0.43	-0.48	0.08	-0.46	-1.12	-0.79	0.47		
TK1039	Cyclic 2,3-diphospoglycerate synthetase_COG2	-0.64	-0.47	-0.55	0.12	-0.21	0.85	0.32	0.75		
TK1040	Hypothetical protein, conserved	-	0.05	-	-	-	-	-	-		
TK1041	Transcription regulator, ArsR family_COG0640	-0.40	-0.39	-0.39	0.00	1.68	-0.24	0.72	1.35		
TK1042	Hypothetical membrane protein, conserved	0.07	0.03	0.05	0.03	-0.17	-0.14	-0.16	0.02		coding
TK1043	Hypothetical protein, conserved_COG3595	-0.02	0.05	0.02	0.06	1.02	0.91	0.96	0.07		
TK1044	Predicted permease, major facilitator superfam	-0.24	-0.55	-0.40	0.21	-	-	-	-		
TK1045	Cobalamin adenosyltransferase_COG2096	0.49	-0.30	0.10	0.56	-	-	-	-		
TK1046	Hypothetical protein, conserved, containing PK	-0.93	-0.84	-0.88	0.06	-0.85	-0.77	-0.81	0.06		
TK1047	Translation initiation factor eIF-2B, delta subu	0.22	0.09	0.16	0.10	-	-	-	-		
TK1048	ATPase, RecA superfamily_COG0467	-0.03	-0.06	-0.04	0.02	-0.06	0.92	0.43	0.70		
TK1049	Methionyl-tRNA synthetase_COG0143	0.21	0.09	0.15	0.09	-	-1.37	-	-		
TK1050	Hypothetical membrane protein, conserved_CO	-	-1.25	-	-	-0.85	-0.95	-0.90	0.07		
TK1051	Hypothetical protein	-1.64	-1.51	-1.57	0.10	-0.92	-1.25	-1.08	0.23		
TK1052	Hypothetical protein	-0.66	-0.42	-0.54	0.17	1.44	0.04	0.74	0.99		
TK1053	Hypothetical membrane protein, conserved, DU	-0.12	-0.34	-0.23	0.16	-	1.50	-	-		
TK1054	N-Acetyltransferase, GNAT family_COG0454	-0.45	-0.14	-0.30	0.22	-	1.68	-	-		
TK1055	Peroxiredoxin, bacterioferritin comigratory prot	-0.40	-0.08	-0.24	0.22	-	-1.03	-	-		
TK1056	Rubrerythrin-related protein_COG1633	-	-0.40	-	-	-1.90	-1.26	-1.58	0.45		
TK1057	Iron(II) uptake regulation protein, frame shift	-0.98	-0.35	-0.67	0.45	-	-0.90	-	-		
TK1058	Iron(II) uptake regulation protein, frame shift	-0.03	-0.16	-0.10	0.09	-	3.89	-	-		
TK1059	Ferritin-related protein_COG2406	-0.49	-0.23	-0.36	0.18	-0.25	-0.51	-0.38	0.19		
TK1060	Hypothetical protein, conserved_COG1633	-0.95	-0.41	-0.68	0.38	-0.48	-0.13	-0.30	0.25		
TK1061	Hypothetical protein, conserved	-0.20	-0.40	-0.30	0.14	-	5.10	-	-		
TK1062	Rubrerythrin-related protein_COG1633	0.27	-0.06	0.10	0.23	-	0.59	-	-		
TK1063	Small-conductance mechanosensitive channel	-1.02	-1.11	-1.07	0.07	-0.48	-1.17	-0.82	0.49		
TK1064	Predicted metallocofactor modifying protein, ra	-0.55	-0.31	-0.43	0.17	-	-	-	-	coding	
TK1065	Molybdopterin converting factor, subunit 1_CO	-	-0.07	-	-	-	-	-	-		
TK1066	Tungsten-containing aldehyde:ferredoxin oxido	-0.09	-0.02	-0.06	0.05	-	1.19	-	-	coding	
TK1067	Hypothetical protein, conserved, containing DU	-0.18	-0.14	-0.16	0.03	-	0.23	-	-		
TK1068	Hypothetical protein, conserved	0.28	0.12	0.20	0.11	-	-	-	-		
TK1069	Hypothetical protein, conserved	0.21	0.03	0.12	0.12	1.41	-0.30	0.55	1.21		
TK1070	Hypothetical protein	0.36	0.11	0.24	0.18	-	2.80	-	-		
TK1071	Phosphodiesterase_COG1524	-0.35	-0.24	-0.30	0.08	-	-	-	-		
TK1072	Hypothetical protein, conserved, DUF103 famil	-0.83	-0.51	-0.67	0.23	-0.32	-0.52	-0.42	0.14		
TK1073	Nucleotidyltransferase_COG1708	0.27	0.10	0.18	0.12	0.32	0.35	0.33	0.03		
TK1074	Hypothetical protein, conserved	-0.64	-0.51	-0.57	0.09	0.91	-0.20	0.36	0.79		
TK1075	Hypothetical protein	0.14	-0.07	0.03	0.15	0.65	0.70	0.67	0.04		
TK1076	Transcription regulator, SpoVT/AbrB family	-	-	-	-	-	-	-	-		
TK1077	SSU ribosomal protein S7_COG0049	0.47	0.48	0.48	0.01	-1.39	-1.39	-1.39	0.00		
TK1078	SSU ribosomal protein S12_COG0048	-0.34	0.03	-0.16	0.26	-	-1.22	-	-		
TK1079	Transcription termination-antitermination facto	0.50	0.32	0.41	0.13	-	-	-	-		
TK1080	LSU ribosomal protein L30E_COG1911	0.23	0.20	0.22	0.02	-1.25	-1.03	-1.14	0.16	coding	
TK1081	DNA-directed RNA polymerase, subunit A''_CO	0.52	0.39	0.46	0.09	-0.89	-1.19	-1.04	0.21	coding	
TK1082	DNA-directed RNA polymerase, subunit A'_CO	-0.31	-0.14	-0.23	0.12	-0.93	-1.06	-1.00	0.09	coding	
TK1083	DNA-directed RNA polymerase, subunit B_CO	0.25	0.14	0.20	0.08	-0.96	-0.92	-0.94	0.03	coding	coding
TK1084	DNA-directed RNA polymerase, subunit H_CO	0.12	0.01	0.07	0.08	-0.20	0.23	0.02	0.30		
TK1085	Protein disulfide oxidoreductase_COG0526	-0.53	-0.49	-0.51	0.03	-	-1.05	-	-		
TK1086	Predicted transcription regulator, ArsR family_C	-0.42	-0.07	-0.25	0.25	-1.49	-0.95	-1.22	0.38		

TK1087	Ferredoxin 2_COG1145	0.20	0.07	0.13	0.09	-	-0.51	-	-		
TK1088	Geranylgeranyl hydrogenase_COG0644	-0.18	-0.07	-0.13	0.07	-2.33	-1.25	-1.79	0.76		
TK1089	Hypothetical protein	-0.59	-0.66	-0.63	0.04	-1.44	-1.12	-1.28	0.23		
TK1090	Hypothetical membrane protein, conserved	-0.19	-0.45	-0.32	0.19	-1.04	-1.70	-1.37	0.46		
TK1091	DNA topoisomerase I; intein_COG0550;COG055	0.22	0.00	0.11	0.16	-	-0.22	-	-		
TK1092	Hypothetical protein, conserved, containing AT	-0.26	-0.27	-0.26	0.01	2.22	0.26	1.24	1.39		
TK1093	Sulfur transfer protein involved in thiamine bios	0.26	0.12	0.19	0.10	-	-	-	-		
TK1094	Alanine aminotransferase_COG0436	0.21	0.13	0.17	0.06	-1.37	-1.20	-1.28	0.11	coding	
TK1095	Hypothetical membrane protein, conserved	-0.79	-0.42	-0.61	0.26	1.52	1.23	1.38	0.20		
TK1096	Hypothetical membrane protein, conserved, DU	-0.87	-0.55	-0.71	0.23	-0.91	0.22	-0.34	0.80		
TK1097	Hypothetical protein, conserved	-0.22	0.03	-0.10	0.17	0.15	0.23	0.19	0.05		
TK1098	LSU ribosomal protein L44E_COG1631	-0.43	-0.25	-0.34	0.13	-1.13	-1.01	-1.07	0.09		
TK1099	SSU ribosomal protein S27E_COG2051	0.28	0.06	0.17	0.16	-	2.62	-	-		
TK1100	Translation initiation factor eIF-2, alpha subuni	0.14	0.05	0.10	0.06	-0.68	-0.19	-0.43	0.34		
TK1101	RNA-binding protein, Nop10p family_COG2260	-0.53	-0.26	-0.39	0.19	0.82	-	-	-	5' (+41)	
TK1102	Hypothetical protein, conserved, DUF75 family	0.32	0.20	0.26	0.09	-0.88	-0.84	-0.86	0.03		
TK1103	ABC-type cobalt transport system, CbiM perm	-0.15	-0.39	-0.27	0.17	-	0.11	-	-		
TK1104	Hypothetical membrane protein, conserved	-0.58	-0.42	-0.50	0.11	-	2.67	-	-		
TK1105	ABC-type cobalt transport system, CbiQ perm	0.21	-0.23	-0.01	0.31	-	-0.20	-	-		
TK1106	ABC-type cobalt transport system, ATPase co	0.61	0.60	0.61	0.01	-	-0.34	-	-	coding	
TK1107	Hypothetical protein, conserved	3.47	3.78	3.62	0.22	1.77	1.80	1.79	0.02		
TK1108	Phosphohexomutase_COG1109	0.27	0.12	0.20	0.11	-0.13	0.55	0.21	0.48		
TK1109	Bifunctional mannose-6-phosphate isomerase/	-0.71	-0.34	-0.53	0.26	-	-0.59	-	-		
TK1110	ADP-dependent glucokinase_COG4809	-0.45	-0.46	-0.46	0.01	-	-0.14	-	-		
TK1111	Archaeal glucose-6-phosphate isomerase_COG	-0.07	-0.10	-0.09	0.02	-	-	-	-		
TK1112	RNA-binding protein, containing KH domain_CO	0.20	-0.13	0.03	0.24	-	-	-	-		
TK1113	Predicted signaling protein, TraB family_COG19	0.12	-0.03	0.04	0.11	0.12	0.85	0.49	0.52		
TK1114	Ribonuclease Z_COG1234	0.20	0.13	0.17	0.05	-	-1.18	-	-		
TK1115	Hypothetical protein, conserved, containing TP	-0.16	-0.18	-0.17	0.01	0.11	-0.40	-0.15	0.36		
TK1116	23S rRNA (uracil-5-)-methyltransferase_COG2	-	0.11	-	-	-	0.24	-	-		
TK1117	Hypothetical protein	-0.26	-0.19	-0.23	0.05	-	-0.62	-	-		
TK1118	Predicted nucleic acid-binding protein, contain	-0.29	-0.57	-0.43	0.20	-	0.64	-	-		5' (+39)
TK1119	6-Pyruvoyl-tetrahydropterin synthase_COG072	0.15	0.07	0.11	0.06	2.59	0.60	1.59	1.41		
TK1120	Hypothetical protein, conserved, DUF192 famil	0.55	0.22	0.39	0.23	-	-0.61	-	-		
TK1121	Prefoldin, alpha subunit_COG1730	-0.37	0.13	-0.12	0.35	-0.27	0.34	0.03	0.43		
TK1122	Prefoldin, beta subunit	-0.19	0.05	-0.07	0.17	-	4.48	-	-		
TK1123	2-Oxoacid:ferredoxin oxidoreductases, gamma	-0.03	0.25	0.11	0.20	-1.41	-0.95	-1.18	0.32		
TK1124	2-Oxoacid:ferredoxin oxidoreductases, beta su	0.59	0.51	0.55	0.05	-0.80	-0.32	-0.56	0.34		
TK1125	2-Oxoacid:ferredoxin oxidoreductases, alpha su	0.06	0.18	0.12	0.09	-0.73	-1.36	-1.05	0.45		
TK1126	2-Oxoacid:ferredoxin oxidoreductases, gamma	0.35	0.41	0.38	0.04	-0.26	-0.57	-0.41	0.22		
TK1127	Hypothetical protein, conserved, DUF103 famil	0.97	0.61	0.79	0.26	-0.39	-0.84	-0.62	0.31		
TK1128	Nucleotidyltransferase	-0.06	0.11	0.02	0.11	-0.78	-1.01	-0.90	0.16		
TK1129	2-Oxoacid:ferredoxin oxidoreductases, beta su	-0.21	0.07	-0.07	0.20	-	-	-	-		
TK1130	2-Oxoacid:ferredoxin oxidoreductases, alpha su	0.22	0.24	0.23	0.01	-0.78	-0.69	-0.73	0.07	coding	
TK1131	2-Oxoacid: ferredoxin oxidoreductase, delta su	-0.14	-0.02	-0.08	0.09	-0.20	-0.77	-0.49	0.40		
TK1132	Hypothetical membrane protein	1.87	1.92	1.89	0.03	0.46	-0.69	-0.12	0.81	5' (-43)	
TK1133	Hypothetical protein	2.03	2.17	2.10	0.10	0.10	0.08	0.09	0.01	5' (+43)	
TK1134	Hypothetical membrane protein	1.40	1.45	1.43	0.03	-0.19	-0.14	-0.16	0.03		
TK1135	Hypothetical protein, conserved, radical SAM s	-0.15	-0.09	-0.12	0.04	-0.55	-0.80	-0.67	0.18		
TK1136	Hypothetical protein, conserved	0.55	0.06	0.31	0.35	0.06	-	-	-		
TK1137	Acid phosphatase SurE homolog_COG0496	-0.21	-0.05	-0.13	0.12	-	0.25	-	-		
TK1138	Hypothetical membrane protein, conserved_CO	0.01	0.02	0.01	0.00	-0.08	0.96	0.44	0.73		
TK1139	ATPase, AAA superfamily_COG0464	-1.01	-0.45	-0.73	0.40	-	0.11	-	-		
TK1140	Seryl-tRNA synthetase_COG0172	0.14	0.05	0.09	0.06	-0.56	-0.92	-0.74	0.25		
TK1141	Endonuclease III (DNA-(apurinic or apyrimidinic	0.08	-0.08	0.00	0.11	-1.24	-1.64	-1.44	0.28		
TK1142	Hypothetical protein, conserved	-0.55	-0.23	-0.39	0.23	0.34	-0.03	0.16	0.27		
TK1143	Transcription regulator, PadR-like family_COG1	0.12	-0.04	0.04	0.12	0.13	-	-	-		
TK1144	ABC-type multidrug transport system, ATPase	-0.52	-0.31	-0.41	0.15	-	-	-	-		
TK1145	ABC-type multidrug transport system, permea	-0.22	-0.17	-0.19	0.04	0.01	-0.90	-0.44	0.64	coding	
TK1146	3-Phosphoglycerate kinase_COG0126	0.47	0.19	0.33	0.20	-	0.05	-	-		
TK1147	Predicted type II restriction endonuclease	0.45	0.31	0.38	0.09	-0.25	0.20	-0.02	0.31		
TK1148	Hypothetical protein, conserved	-0.29	-0.21	-0.25	0.05	-0.23	-0.91	-0.57	0.48		
TK1149	Methylmalonyl-CoA mutase, N-terminus of larg	0.25	0.24	0.24	0.01	-0.06	-0.30	-0.18	0.18		
TK1150	Hypothetical membrane protein, conserved	0.05	-0.01	0.02	0.04	1.56	0.70	1.13	0.61	coding	
TK1151	ABC-type transport system, permease compor	0.09	-0.20	-0.06	0.20	-	-0.68	-	-		
TK1152	ABC-type multidrug transport system, ATPase	0.78	-0.11	0.34	0.63	1.19	0.01	0.60	0.83	coding	
TK1153	Hypothetical protein, conserved_COG1236	-0.37	-0.11	-0.24	0.18	-	-	-	-		
TK1154	Hypothetical protein	0.20	0.20	0.20	0.00	-	-	-	-		
TK1155	Small heat shock protein_COG0071	0.47	0.41	0.44	0.04	-	0.38	-	-		
TK1156	Hypothetical protein	-0.59	-0.59	-0.59	0.00	-	-1.80	-	-		
TK1157	CDC48/VCP homolog, AAA superfamily_COG0	0.42	0.64	0.53	0.15	-0.53	-0.52	-0.53	0.01	coding	coding
TK1158	Predicted endonuclease-methyltransferase fus	0.88	0.79	0.84	0.06	0.04	-0.13	-0.05	0.12	coding	
TK1159	Hypothetical protein	0.74	0.59	0.66	0.10	-	0.72	-	-		
TK1160	Hypothetical membrane protein	1.39	1.14	1.27	0.18	-1.52	-	-	-	5' (-2)	
TK1161	Dihydropteroate synthase_COG0294	0.70	0.77	0.73	0.05	-0.22	-0.89	-0.55	0.47		
TK1162	Hypothetical membrane protein, conserved, DU	0.08	0.05	0.06	0.02	-0.22	-0.31	-0.26	0.07		
TK1163	Hypothetical protein, conserved	-0.21	-0.03	-0.12	0.13	0.04	0.48	0.26	0.32		
TK1164	Predicted endopeptidase IV, S49 family_COG06	-0.06	-0.17	-0.12	0.08	-	-0.16	-	-	coding	coding
TK1165	Predicted AP endonuclease_COG1082	0.16	0.14	0.15	0.01	-	-0.13	-	-		
TK1166	Hypothetical protein, conserved	-0.61	-0.34	-0.47	0.19	-0.69	-0.89	-0.79	0.14		
TK1167	DNA-directed RNA polymerase, subunit L_COG	-0.22	0.15	-0.03	0.26	-0.69	-0.64	-0.67	0.04		
TK1168	Hypothetical protein, conserved_COG3286	0.60	0.43	0.52	0.12	0.98	-0.41	0.29	0.98		
TK1169	RNA-binding protein, containing S1 domain_CO	-0.41	-0.11	-0.26	0.21	-1.01	-0.25	-0.63	0.53		
TK1170	Threonyl-tRNA synthetase_COG0441	0.29	0.09	0.19	0.14	-1.70	-1.40	-1.55	0.21		
TK1171	Hypothetical protein, conserved, N-truncation	-0.10	-0.11	-0.10	0.01	0.38	-0.33	0.03	0.51		
TK1172	TBP-interacting protein	0.05	0.05	0.05	0.00	-1.30	-1.48	-1.39	0.13		
TK1173	Undecaprenyl diphosphate synthase_COG0020	-0.82	-0.67	-0.75	0.10	0.37	0.18	0.28	0.14		
TK1174	Predicted acetyltransferase, isoleucine patch s	-1.49	-1.09	-1.29	0.28	-1.11	-1.47	-1.29	0.25		
TK1175	Archaeal type Holliday junction resolvase_COG	-0.30	-0.31	-0.31	0.01	-0.21	1.56	0.68	1.25		
TK1176	Hypothetical membrane protein, conserved	-0.55	-0.46	-0.50	0.06	-	1.04	-	-		
TK1177	Deblocking aminopeptidase_COG1363	0.10	0.06	0.08	0.03	-1.33	-1.42	-1.38	0.06		

TK1178	Hypothetical protein, conserved_COG1913	0.11	-0.04	0.03	0.11	1.41	3.77	2.59	1.67		
TK1179	Adenylate cyclase, class 2_COG1437	-0.53	-0.35	-0.44	0.13	0.62	-0.08	0.27	0.50		
TK1180	Hypothetical protein, conserved	-0.72	-0.46	-0.59	0.18	-	0.93	-	-		
TK1181	ABC-type cobalt transport system, ATPase co	0.05	-0.15	-0.05	0.13	-	-0.22	-	-		
TK1182	Trk-type pottasium transport system, membra	-0.43	-0.34	-0.38	0.06	-0.64	1.88	0.62	1.78		
TK1183	Methionyl aminopeptidase_COG0024	0.16	-0.14	0.01	0.21	-0.69	-0.39	-0.54	0.21		
TK1184	Hypothetical protein, conserved	0.17	0.11	0.14	0.04	0.98	1.07	1.02	0.06		
TK1185	Predicted nucleic acid-binding protein, contain	-0.60	-0.55	-0.57	0.03	-	5.11	-	-		coding
TK1186	Hypothetical protein, conserved, containing CB	0.22	0.08	0.15	0.10	0.52	-0.11	0.20	0.44		
TK1187	Hypothetical membrane protein, conserved, co	0.33	0.11	0.22	0.15	3.19	0.84	2.01	1.67		
TK1188	Sugar-phosphate nucleotydyltransferase_COG1	-0.57	-0.33	-0.45	0.17	1.38	2.80	2.09	1.01		
TK1189	Bacitracin resistance protein BacA homolog	-0.43	-0.45	-0.44	0.02	-	-	-	-	coding	
TK1190	Predicted GTPase, containing NOG1 domain_C	0.10	-0.12	-0.01	0.15	-	1.05	-	-		
TK1191	SSU ribosomal protein S8E_COG2007	-0.06	-0.13	-0.09	0.05	-1.49	-1.41	-1.45	0.06		
TK1192	Hypothetical membrane protein, conserved	0.29	0.52	0.40	0.17	-0.49	0.15	-0.17	0.45		
TK1193	CTP synthase (UTP--ammonia ligase)_COG050	-0.31	-0.45	-0.38	0.10	-0.82	-0.48	-0.65	0.24	coding	
TK1194	Hypothetical protein, conserved, DUF555 famil	0.49	0.37	0.43	0.09	-0.59	-0.69	-0.64	0.07		
TK1195	Hypothetical protein, conserved, DUF357 famil	0.49	0.46	0.47	0.02	-0.20	-0.73	-0.46	0.38		
TK1196	Hypothetical protein, conserved	0.55	0.08	0.31	0.33	-0.58	0.16	-0.21	0.52		
TK1197	Hypothetical protein, conserved	0.55	0.25	0.40	0.21	-	-0.85	-	-		
TK1198	Organic radical activating enzyme, radical SAM	-0.12	-0.02	-0.07	0.07	3.72	0.66	2.19	2.16		
TK1199	TBP-interacting protein Tip49 homolog_COG12	-0.50	-0.22	-0.36	0.20	-1.05	-0.42	-0.74	0.44		
TK1200	Hypothetical membrane protein	2.31	1.97	2.14	0.24	0.59	1.23	0.91	0.45	coding	
TK1201	Hypothetical protein, conserved	4.16	3.89	4.03	0.19	1.01	0.58	0.79	0.30		
TK1202	Hypothetical protein, conserved, flame shift	2.08	2.24	2.16	0.12	-0.07	0.49	0.21	0.40		
TK1203	Hypothetical protein, conserved, flame shift	0.00	-0.13	-0.06	0.09	-	0.11	-	-		
TK1204	Hypothetical protein, conserved_COG5423	0.59	0.30	0.45	0.21	-	-0.47	-	-		
TK1205	Phospholipid-binding protein, PBP family_COG1	0.73	0.42	0.58	0.22	1.06	0.67	0.86	0.28		
TK1206	Hypothetical membrane protein, conserved	0.70	0.29	0.49	0.29	-	1.83	-	-		
TK1207	Hypothetical protein, conserved	-0.46	-0.21	-0.33	0.18	-0.38	-0.45	-0.42	0.05		
TK1208	Glutaredoxin-related protein_COG0526	-0.20	-0.22	-0.21	0.01	-0.42	-0.13	-0.27	0.20		
TK1209	Transmembrane electron transport protein_CO	-0.04	-0.36	-0.20	0.22	-	-0.71	-	-		
TK1210	Transcription regulator, Lrp/AsnC family_COG1	-0.45	-0.49	-0.47	0.03	0.47	0.36	0.42	0.08		
TK1211	Aminotransferase, class III_COG0160	-0.37	-0.35	-0.36	0.01	-	2.24	-	-		
TK1212	Xanthine/uracil permease_COG2233	-	-0.42	-	-	-	-1.22	-	-		
TK1213	Hypothetical membrane protein, conserved, DU	-0.04	0.39	0.18	0.30	0.97	-	-	-		
TK1214	Membrane bound hydrogenase, 4Fe-4S cluster	0.04	-0.14	-0.05	0.13	-	-	-	-		
TK1215	Membrane bound hydrogenase, NiFe-hydrogena	0.11	-0.08	0.01	0.14	-	-0.09	-	-		
TK1216	Membrane bound hydrogenase, NiFe-hydrogena	0.66	0.34	0.50	0.22	-	-1.10	-	-		
TK1217	Membrane bound hydrogenase, NiFe-hydrogena	0.32	0.14	0.23	0.13	-1.26	-1.02	-1.14	0.17		
TK1218	Membrane bound hydrogenase, MbxM subunit_C	-	-0.17	-	-	-1.35	-1.09	-1.22	0.18		
TK1219	Membrane bound hydrogenase, MbxH' subunit	-0.42	-0.32	-0.37	0.07	-1.18	-0.65	-0.91	0.38		
TK1220	Membrane bound hydrogenase, MbxH subunit (	-0.24	-0.23	-0.23	0.01	-	-1.65	-	-	coding	
TK1221	Membrane bound hydrogenase, MbxG subunit (	0.07	-0.24	-0.09	0.22	-	-1.83	-	-		
TK1222	Membrane bound hydrogenase, MbxF subunit (	-0.05	-0.26	-0.15	0.15	-0.58	0.12	-0.23	0.49	coding	
TK1223	Membrane bound hydrogenase, MbxD subunit (	-0.29	-0.29	-0.29	0.00	-3.65	-1.71	-2.68	1.37		
TK1224	Membrane bound hydrogenase, MbxC subunit (	-0.21	-0.19	-0.20	0.01	0.05	-0.68	-0.32	0.52	coding	
TK1225	Membrane bound hydrogenase, MbxB subunit (	0.14	-0.06	0.04	0.14	-	-	-	-		
TK1226	Membrane bound hydrogenase, MbxA subunit (	0.04	0.00	0.02	0.03	-1.15	-1.10	-1.13	0.04		
TK1227	Predicted regulator of amino acid metabolism, (	0.48	0.24	0.36	0.16	-1.13	-0.60	-0.86	0.37		
TK1228	Probable molybdenum cofactor biosynthesis pr	-0.35	-0.42	-0.38	0.05	-	-	-	-		
TK1229	Hypothetical protein	-0.78	-0.55	-0.66	0.16	-0.26	0.61	0.18	0.62		
TK1230	UDP-N-acetylglucosamine 2-epimerase_COG0	-0.67	-0.29	-0.48	0.26	-0.70	-0.13	-0.42	0.40		
TK1231	UDP-N-acetyl-D-mannosaminuronate dehydro	0.30	0.40	0.35	0.08	-0.66	-0.76	-0.71	0.07		
TK1232	Hypothetical protein, conserved, DUF354 famil	0.12	0.41	0.27	0.20	-	0.44	-	-		
TK1233	Hypothetical membrane protein, conserved, DU	0.80	0.81	0.80	0.00	1.08	0.90	0.99	0.13		
TK1234	Lipoate-protein ligase A, C-terminal section_C	1.33	1.19	1.26	0.10	1.35	1.17	1.26	0.13		
TK1235	Arginyl-tRNA synthetase_COG0018	-0.36	-0.18	-0.27	0.13	-0.41	-1.44	-0.93	0.73	coding	
TK1236	Archaeal ATPase_COG1672	-0.60	-0.57	-0.58	0.03	-0.70	-	-	-		
TK1237	Probable dihydrodipicolinate synthase_COG032	-0.72	-0.33	-0.53	0.28	-	0.64	-	-		
TK1238	Hypothetical protein, conserved	0.09	-0.24	-0.08	0.23	-	-2.34	-	-		
TK1239	Peptide chain release factor eRF1_COG1503	0.33	0.18	0.25	0.11	-0.42	-0.97	-0.69	0.39		
TK1240	Hypothetical membrane protein, conserved	-0.06	-0.02	-0.04	0.03	-	-	-	-		
TK1241	Hypothetical protein, conserved	0.25	0.05	0.15	0.14	-	-0.69	-	-		
TK1242	Hypothetical protein, conserved	-0.12	-0.32	-0.22	0.14	-	-3.42	-	-		
TK1243	Hypothetical protein, conserved	0.10	-0.01	0.05	0.08	-0.40	-0.05	-0.23	0.25		
TK1244	Hypothetical protein	0.06	0.29	0.18	0.16	-	-0.37	-	-		
TK1245	Hypothetical protein, conserved	0.15	0.33	0.24	0.13	-0.24	-0.20	-0.22	0.02		
TK1246	Hypothetical protein, conserved	-0.48	-0.27	-0.37	0.15	-	2.85	-	-		
TK1247	Membrane-associated metallopeptidase, M50 f	-0.17	-0.26	-0.22	0.06	-1.69	-1.05	-1.37	0.45	coding	
TK1248	Hypothetical protein, conserved, DUF126 famil	-0.17	-0.08	-0.13	0.06	-1.26	-1.73	-1.49	0.33		
TK1249	Hypothetical protein, conserved, DUF521 famil	-0.09	-0.21	-0.15	0.09	-	-	-	-		
TK1250	Intein/rRNA intron-related DNA endonuclease_	1.52	1.52	1.52	0.00	0.12	-0.06	0.03	0.13		
TK1251	SSU ribosomal protein S15P_COG0184	0.42	0.36	0.39	0.04	-1.27	-1.07	-1.17	0.14		
TK1252	ssDNA-specific exonuclease_COG0608	0.35	0.23	0.29	0.08	-0.85	-0.72	-0.78	0.09		
TK1253	Hypothetical protein, conserved	0.28	0.13	0.21	0.11	-	-0.98	-	-		
TK1254	SSU ribosomal protein S3AE_COG1890	-0.82	-0.23	-0.52	0.42	-1.52	-1.39	-1.45	0.09		
TK1255	Hypothetical protein, conserved	0.43	-0.05	0.19	0.34	-	3.91	-	-		
TK1256	Predicted nucleic acid-binding protein, contain	-0.57	-0.54	-0.56	0.02	-0.39	-0.09	-0.24	0.21		
TK1257	RNA-binding protein, containing THUMP domai	-0.62	-0.66	-0.64	0.02	0.12	0.18	0.15	0.04		
TK1258	Hypothetical membrane protein, conserved, DU	-0.33	-0.19	-0.26	0.10	-0.37	-	-	-		
TK1259	Predicted transcription regulator, Lrp/AsnC fa	-1.60	1.27	-0.17	2.03	-	1.53	-	-		
TK1260	Nucleotide pyrophosphohydrolase_COG1694	-0.04	-0.16	-0.10	0.09	0.68	-	-	-		
TK1261	Transcription regulator, ArsR family_COG0640	0.14	0.32	0.23	0.13	-	0.81	-	-		
TK1262	Predicted metalloprotease, containing Jab1/MI	-0.38	-0.36	-0.37	0.01	0.49	-0.94	-0.23	1.01		
TK1263	Hypothetical protein, conserved	-0.17	-0.05	-0.11	0.08	-0.26	-0.56	-0.41	0.21		coding
TK1264	ATP-dependent protease Lon_COG1067	-0.25	-0.33	-0.29	0.05	-1.25	-1.29	-1.27	0.03		coding
TK1265	Hypothetical membrane protein	0.12	-0.17	-0.02	0.21	0.62	1.82	1.22	0.85		
TK1266	Predicted transcription regulator, containing CI	-1.00	-0.54	-0.77	0.33	-1.99	-	-	-		
TK1267	Permease, drug/metabolite transporter (DMT)	-0.29	-0.19	-0.24	0.07	-	1.31	-	-		coding
TK1268	Hypothetical protein, conserved	0.02	-0.11	-0.05	0.09	0.17	2.97	1.57	1.98		

TK1269	Predicted phosphoesterase, DHH family, fused	-0.25	-0.14	-0.20	0.07	-	-0.63	-	-		
TK1270	Hypothetical protein, conserved, containing PR	0.13	-0.04	0.04	0.12	-	-	-	-		
TK1271	Hypothetical membrane protein	-0.56	-0.24	-0.40	0.23	-	-	-	-		
TK1272	Predicted transcription regulator, containing C	-0.09	-0.20	-0.14	0.07	-0.67	-0.82	-0.74	0.10		
TK1273	SAM-dependent methyltransferase, UbiE/COQ	-0.24	-0.59	-0.41	0.25	-	-	-	-		
TK1274	Valyl-tRNA synthetase_COG0525	0.20	0.00	0.10	0.15	-	-1.44	-	-		
TK1275	Predicted RNA-binding protein, CRS1/YhbY fa	0.55	0.36	0.46	0.14	-	-0.95	-	-		
TK1276	SSU ribosomal protein S19E_COG2238	-0.19	-0.13	-0.16	0.04	-1.10	-0.95	-1.03	0.11		
TK1277	Hypothetical membrane protein	4.03	3.38	3.70	0.45	-	0.45	-	-	5' (+15)	
TK1278	Double-stranded DNA-binding protein_COG211	-0.20	-0.19	-0.20	0.01	-1.77	-1.13	-1.45	0.46		
TK1279	Hypothetical protein	-0.19	-0.19	-0.19	0.00	0.27	-0.71	-0.22	0.69		
TK1280	Transcription initiation factor IIB_COG1405	-0.26	-0.16	-0.21	0.07	-0.57	-1.00	-0.78	0.30		
TK1281	Flap structure-specific endonuclease_COG025	-0.81	-0.37	-0.59	0.32	-0.30	-0.23	-0.26	0.05		
TK1282	Molybdenum cofactor biosynthesis protein Moe	-0.40	-0.01	-0.20	0.28	-0.26	-0.34	-0.30	0.06		
TK1283	Predicted ATPase, PP-loop superfamily_COG2	0.71	0.46	0.58	0.18	-	-0.66	-	-		
TK1284	Intracellular protease I_COG0693	-0.80	-0.73	-0.76	0.05	-0.99	-1.66	-1.33	0.47		
TK1285	Transcription regulator, Lrp/AsnC family_COG1	-	-0.39	-	-	-1.82	-1.42	-1.62	0.28		
TK1286	Predicted GTPase, GTP1/OBG family, containi	0.05	0.13	0.09	0.06	1.37	-0.81	0.28	1.54		
TK1287	Uracil phosphoribosyltransferase_COG0035	-0.28	-0.43	-0.36	0.10	-	-0.91	-	-		
TK1288	Sodium-driven multidrug efflux pump protein_C	-0.32	0.00	-0.16	0.23	3.03	-	-	-		
TK1289	Sodium-driven multidrug efflux pump protein_C	-	0.07	-	-	-	0.85	-	-		
TK1290	Predicted nucleic acid-binding protein, containi	-0.03	-0.16	-0.10	0.10	-0.36	-1.04	-0.70	0.48		
TK1291	Predicted transcription regulator, SpoVT/AbrB	0.06	-0.06	0.00	0.09	-	-	-	-		
TK1292	Phosphoenolpyruvate synthetase (pyruvate, wa	0.36	0.19	0.27	0.12	-1.42	-1.07	-1.24	0.25	coding	coding
TK1293	Putative membrane-bound dolichyl-phosphate-	-0.04	-0.40	-0.22	0.25	-0.93	-0.83	-0.88	0.07		
TK1294	Hypothetical membrane protein, conserved, DU	-0.75	-0.73	-0.74	0.02	-	-	-	-		
TK1295	Predicted thiol protease	-0.30	-0.43	-0.37	0.09	-1.42	-1.88	-1.65	0.32	coding	
TK1296	Hypothetical protein, conserved, DUF424 family	0.36	0.01	0.19	0.24	-0.49	0.02	-0.23	0.37		
TK1297	Nonsense-mediated mRNA decay protein NMD	0.17	0.09	0.13	0.05	-	-0.09	-	-		
TK1298	Hypothetical protein, conserved, DUF1464 fam	0.12	0.05	0.09	0.05	-0.44	-0.76	-0.60	0.23		
TK1299	NADH oxidase_COG0446	0.15	0.06	0.11	0.07	-	-	-	-	coding	
TK1300	Hypothetical membrane protein, conserved_CO	-	-0.05	-	-	-	1.22	-	-		
TK1301	Probable ATP-NAD kinase_COG3199	-0.35	-0.08	-0.21	0.19	1.32	0.73	1.02	0.42		
TK1302	Hypothetical membrane protein, conserved	0.69	0.57	0.63	0.09	0.32	0.18	0.25	0.10		
TK1303	Hypothetical protein, conserved	2.36	2.10	2.23	0.18	-0.02	0.62	0.30	0.46	5' (-55)	5' (+41)
TK1304	Hypothetical protein, conserved	2.63	2.40	2.52	0.16	1.34	0.49	0.91	0.60	5' (-85)	
TK1305	Translation initiation factor IF-2; intein_COG05	-0.57	-0.21	-0.39	0.25	-1.51	0.03	-0.74	1.09		
TK1306	Hypothetical membrane protein	-0.10	-0.21	-0.16	0.08	3.10	0.76	1.93	1.66		
TK1307	Nucleoside diphosphate kinase_COG0105	0.38	0.36	0.37	0.01	-0.96	-0.87	-0.91	0.07	coding	
TK1308	Hypothetical protein	2.02	1.99	2.01	0.02	-1.12	-0.50	-0.81	0.44	5' (-38)	
TK1309	LSU ribosomal protein L24E_COG2075	0.15	0.21	0.18	0.05	-	-0.05	-	-		
TK1310	SSU ribosomal protein S28E_COG2053	0.62	0.41	0.52	0.15	-1.17	-1.31	-1.24	0.10		
TK1311	LSU ribosomal protein L7AE_COG1358	0.28	0.27	0.28	0.01	-1.58	-1.15	-1.36	0.30	coding	
TK1312	Hypothetical protein, conserved, containing V4	-0.38	-0.40	-0.39	0.01	1.52	-0.26	0.63	1.26		
TK1313	Hypothetical protein, conserved_COG1326	-0.67	-0.50	-0.58	0.12	0.13	-1.36	-0.61	1.06		
TK1314	Predicted ATPase, AAA superfamily_COG1373	-0.16	-0.04	-0.10	0.08	-	-	-	-		
TK1315	3'-Phosphoadenosine 5'-phosphosulfate reduc	-0.34	-0.19	-0.26	0.10	-	0.53	-	-	5' (-104)	
TK1316	Predicted membrane protease subunit, stomati	3.47	3.37	3.42	0.07	1.34	0.69	1.02	0.46	5' (-14)	
TK1317	Hypothetical membrane protein, conserved_CO	2.37	2.42	2.40	0.03	-0.08	-0.03	-0.06	0.03		
TK1318	Thymidine kinase_COG1435	1.39	1.12	1.26	0.18	0.55	-0.11	0.22	0.47	coding	
TK1319	LSU ribosomal protein L39E_COG2167	0.50	0.42	0.46	0.06	-1.06	-1.03	-1.05	0.02		
TK1320	LSU ribosomal protein L31E_COG2097	0.49	0.36	0.42	0.09	-0.86	-0.55	-0.70	0.21		
TK1321	Translation initiation factor eIF-6_COG1976	0.38	0.29	0.34	0.06	-0.27	-0.64	-0.45	0.26		
TK1322	LSU ribosomal protein L20A_COG2157	-0.45	-0.19	-0.32	0.18	-1.33	-1.32	-1.33	0.00		
TK1323	Glycosyltransferase, family 4_COG0438	-0.44	-0.58	-0.51	0.10	-	-1.25	-	-		
TK1324	4-Hydroxybenzoate octaprenyltransferase_CO	-0.90	-0.54	-0.72	0.25	4.75	1.24	3.00	2.48		
TK1325	Ferredoxin:NADP oxidoreductase, alpha subuni	-0.27	0.14	-0.06	0.28	-	-2.02	-	-	coding	
TK1326	Ferredoxin:NADP oxidoreductase, beta subunit	-0.29	-0.17	-0.23	0.08	-1.78	-1.90	-1.84	0.08		
TK1327	Hypothetical membrane protein	0.14	0.02	0.08	0.08	1.22	1.96	1.59	0.52		
TK1328	tRNA (1-methyladenosine) methyltransferase_C	0.11	-0.04	0.04	0.11	-0.37	0.09	-0.14	0.33		
TK1329	Hypothetical protein, conserved, DUF257 family	-1.00	-0.66	-0.83	0.24	2.70	2.01	2.35	0.49		
TK1330	Signal recognition particle, SRP19 subunit_COG	-0.55	-0.66	-0.61	0.08	-0.37	-0.77	-0.57	0.28		
TK1331	Predicted transcription regulator, Lrp/AsnC fa	0.07	0.31	0.19	0.17	-0.73	-0.38	-0.55	0.25		
TK1332	RNA helicase Ski2 homolog; intein_COG1204	0.03	-0.07	-0.02	0.07	-0.71	-0.57	-0.64	0.10	coding	
TK1333	Hypothetical membrane protein, conserved	-0.81	-0.67	-0.74	0.10	0.76	-	-	-		
TK1334	Dephospho-CoA kinase_COG0237	-0.60	-0.28	-0.44	0.22	-	-0.54	-	-		
TK1335	Hypothetical protein, conserved, DUF54 family_	-0.81	-0.26	-0.54	0.38	-	-0.39	-	-		
TK1336	ABC-type sodium efflux pump system, permea	-0.14	-0.03	-0.08	0.08	-	-0.03	-	-		
TK1337	ABC-type sodium efflux pump system, ATPase	-0.40	-0.42	-0.41	0.01	4.73	1.24	2.98	2.47		
TK1338	Hypothetical membrane protein, conserved	0.25	-0.14	0.06	0.28	-	-	-	-		
TK1339	Predicted transcription regulator, containing D	-0.58	-0.44	-0.51	0.10	-	-	-	-		
TK1340	Hypothetical membrane protein, conserved	-0.35	-0.35	-0.35	0.00	-	0.51	-	-		
TK1341	Hypothetical membrane protein	-0.03	-0.30	-0.17	0.19	-	1.22	-	-		
TK1342	Predicted integrase, C-fragment	-1.54	-0.90	-1.22	0.45	0.22	0.38	0.30	0.11		
TK1343	Predicted nucleic acid-binding protein, contain	-0.40	-0.49	-0.45	0.07	0.56	-0.21	0.17	0.54		
TK1344	Hypothetical protein	-0.53	-0.28	-0.40	0.18	0.32	0.43	0.38	0.08		
TK1345	Hypothetical protein	-	-0.64	-	-	-	-1.77	-	-	coding	
TK1346	Hypothetical protein	-0.79	-0.59	-0.69	0.14	-	-	-	-		
TK1347	Hypothetical protein	-0.99	-0.61	-0.80	0.27	-	-0.07	-	-		
TK1348	Hypothetical protein	-0.63	-0.61	-0.62	0.01	-	-	-	-		
TK1349	Hypothetical protein, conserved	-0.06	-0.10	-0.08	0.03	0.91	3.51	2.21	1.84		
TK1350	Hypothetical protein, containing leucine zipper	-0.47	-0.33	-0.40	0.10	-	-	-	-		
TK1351	Hypothetical membrane protein	-0.45	-0.50	-0.48	0.04	-	0.53	-	-		
TK1352	Hypothetical protein	0.25	0.07	0.16	0.13	-	3.73	-	-		5' (-33)
TK1353	Hypothetical protein	-	0.15	-	-	-	-	-	-		
TK1354	Hypothetical protein	-0.13	-0.13	-0.13	0.00	-	-	-	-		
TK1355	Hypothetical membrane protein	-	0.03	-	-	-	-	-	-		
TK1356	Predicted ATPase, AAA superfamily	-0.52	-0.31	-0.42	0.14	-	2.85	-	-		
TK1357	Hypothetical protein	-0.42	-0.33	-0.38	0.07	-	0.61	-	-		
TK1358	Hypothetical protein	0.38	0.03	0.21	0.25	-	-	-	-		
TK1359	Hypothetical protein	-1.01	-0.45	-0.73	0.40	-	-	-	-		

TK1360	Hypothetical protein	-0.42	-0.39	-0.40	0.02	1.06	1.42	1.24	0.25		coding
TK1361	DNA replication licensing factor, MCM2/3/5 fa	-0.70	-0.35	-0.53	0.25	0.15	0.56	0.36	0.29		
TK1362	Hypothetical membrane protein	-0.07	-0.25	-0.16	0.13	-	0.79	-	-		
TK1363	Hypothetical protein	0.49	0.06	0.28	0.30	-	3.35	-	-		
TK1364	Hypothetical protein	-0.45	-0.40	-0.42	0.04	-	-	-	-		
TK1365	Hypothetical protein	0.16	0.17	0.17	0.01	-	-	-	-		
TK1366	Hypothetical protein	-0.61	-0.53	-0.57	0.05	-	-	-	-		
TK1367	Hypothetical protein	-0.11	-0.37	-0.24	0.18	-	-0.05	-	-		
TK1368	Hypothetical protein	-0.56	-0.34	-0.45	0.16	-	-	-	-		
TK1369	Hypothetical protein, conserved	-0.23	0.16	-0.04	0.27	-	-	-	-		
TK1370	Hypothetical protein	0.55	0.37	0.46	0.12	-	-	-	-		
TK1371	Hypothetical protein	-	-0.03	-	-	-	-	-	-		
TK1372	Predicted transcription regulator, SpoVT/AbrB	-0.27	-0.07	-0.17	0.14	-	0.88	-	-		
TK1373	Hypothetical protein	0.25	0.27	0.26	0.01	2.87	2.41	2.64	0.32		
TK1374	Hypothetical protein, conserved	0.59	0.39	0.49	0.14	-	-0.04	-	-		
TK1375	Hypothetical membrane protein	0.20	-0.03	0.08	0.16	0.98	1.23	1.10	0.18		
TK1376	Hypothetical protein	0.48	0.32	0.40	0.12	0.15	0.11	0.13	0.03		
TK1377	Hypothetical protein	-0.11	0.05	-0.03	0.11	0.36	0.21	0.29	0.10		
TK1378	Predicted integrase, N-fragment	0.38	0.08	0.23	0.22	0.61	-0.17	0.22	0.55		
TK1379	Glycine cleavage system protein P (pyridoxal-b	-0.03	0.01	-0.01	0.03	-0.50	-0.72	-0.61	0.16		
TK1380	Glycine cleavage system protein P (pyridoxal-b	0.09	0.06	0.08	0.02	-0.41	-1.31	-0.86	0.63	coding	
TK1381	Hypothetical protein	-0.36	-0.39	-0.38	0.02	-	0.38	-	-		
TK1382	Dopamine beta hydroxylase-related protein, co	-0.15	-0.24	-0.19	0.07	-	0.33	-	-		
TK1383	Hydrolase, HAD superfamily_COG1011	0.00	0.00	0.00	0.00	0.74	-0.65	0.04	0.98		
TK1384	Hypothetical protein	0.35	-0.16	0.10	0.36	-0.92	-0.55	-0.73	0.26		
TK1385	Hypothetical protein, conserved	-0.27	-0.42	-0.35	0.10	2.91	6.07	4.49	2.24		
TK1386	Metallophosphoesterase, calcineurin superfamil	-0.35	-0.48	-0.42	0.09	0.54	0.51	0.53	0.02		
TK1387	Hypothetical membrane protein, conserved_CO	-0.70	-0.12	-0.41	0.41	-0.66	-0.82	-0.74	0.11		
TK1388	Hypothetical protein, conserved	0.04	-0.12	-0.04	0.11	-	1.87	-	-		
TK1389	Hypothetical protein	-0.21	-0.18	-0.19	0.02	-2.98	0.62	-1.18	2.55		
TK1390	Hypothetical protein, conserved	5.71	5.26	5.49	0.32	2.77	2.62	2.70	0.11	5' (+6)	
TK1391	Molybdopterin oxidoreductase, 4Fe-4S cluster	1.35	1.48	1.41	0.09	3.08	2.19	2.63	0.63		
TK1392	NADH oxidase_COG0446	1.80	1.24	1.52	0.39	-	0.91	-	-		
TK1393	Anaerobic glycerol 3-phosphate dehydrogenas	0.04	0.13	0.08	0.07	-0.54	-0.08	-0.31	0.32		
TK1394	Hypothetical protein	1.19	1.20	1.19	0.01	-	-	-	-		
TK1395	Predicted ATP-dependent endonuclease, OLD	1.26	0.62	0.94	0.45	-	-	-	-		
TK1396	Glycerol kinase_COG0554	-0.16	-0.15	-0.16	0.01	-0.24	0.23	-0.01	0.33	coding	coding
TK1397	Glycerophosphoryl diester phosphodiesterase_(	-0.37	-0.12	-0.24	0.18	-	-0.20	-	-		
TK1398	Glycerophosphoryl diester phosphodiesterase_(	-0.42	-0.45	-0.43	0.02	0.33	1.65	0.99	0.93		
TK1399	Predicted permease, major facilitator superfam	-0.38	-0.62	-0.50	0.17	-0.33	-0.76	-0.54	0.31		
TK1400	Predicted permease, major facilitator superfam	-0.08	-0.36	-0.22	0.19	-	0.29	-	-	coding	
TK1401	Hydrolase, alpha/beta superfamily_COG1073	0.11	-0.04	0.03	0.10	-	-	-	-	coding	
TK1402	Polysaccharide deacetylase_COG3233	1.82	1.60	1.71	0.16	1.30	2.93	2.12	1.16	5' (-51)	
TK1403	Thymidylate kinase_COG0125	-0.46	-0.22	-0.34	0.17	0.13	-0.63	-0.25	0.54		
TK1404	Phosphomannomutase-related protein_COG110	-0.51	-0.17	-0.34	0.24	-0.75	-0.47	-0.61	0.20		
TK1405	Phosphoenolpyruvate carboxykinase (GTP)_CO	-0.61	-0.25	-0.43	0.26	-1.81	-1.73	-1.77	0.06		
TK1406	Maltodextrin phosphorylase_COG0058	-0.04	-0.15	-0.10	0.08	-	-	-	-	coding	
TK1407	Hypothetical membrane protein, conserved	1.22	1.15	1.18	0.05	-	1.31	-	-	coding	
TK1408	Glutamyl-tRNA synthetase_COG0008	0.15	0.32	0.24	0.12	-0.22	-0.29	-0.25	0.05		
TK1409	Hypothetical membrane protein	1.69	1.44	1.56	0.18	-	-	-	-	5' (+30)	
TK1410	DnaG-related protein, containing Toprim domai	-0.18	-0.09	-0.13	0.06	-0.84	-1.31	-1.08	0.33	coding	
TK1411	DnaG-related small protein, containing Toprim	0.07	-0.05	0.01	0.09	-1.62	-0.45	-1.03	0.83		
TK1412	Hypothetical protein, conserved, radical SAM s	0.08	-0.22	-0.07	0.21	-	0.29	-	-		
TK1413	Archaeal histone A_COG2036	-0.07	-0.01	-0.04	0.04	-0.69	-0.28	-0.49	0.29	coding	
TK1414	Deoxycytidine triphosphate deaminase_COG07	-0.80	-0.36	-0.58	0.31	-	-0.09	-	-		
TK1415	LSU ribosomal protein L12A_COG2058	0.62	0.49	0.55	0.09	-	-	-	-	5' (+31)	
TK1416	LSU ribosomal protein L10E_COG0244	-0.12	-0.13	-0.13	0.01	-1.68	-1.90	-1.79	0.16	coding	
TK1417	LSU ribosomal protein L1P_COG0081	0.34	-0.15	0.10	0.35	-1.41	-1.23	-1.32	0.12		
TK1418	LSU ribosomal protein L11P_COG0080	-0.40	-0.32	-0.36	0.05	-1.47	-1.49	-1.48	0.02		
TK1419	Transcription antitermination protein_COG0250	-0.04	-0.09	-0.07	0.03	-1.15	-1.03	-1.09	0.08		
TK1420	Preprotein translocase, SecE subunit_COG244	0.10	0.04	0.07	0.04	-	-0.40	-	-		
TK1421	Cell division GTPase_COG0206	-0.43	-0.34	-0.39	0.06	-1.67	-0.77	-1.22	0.64		
TK1422	Hypothetical protein, conserved, DUF516 family	-0.44	-0.32	-0.38	0.09	-	-0.70	-	-		
TK1423	Hypothetical protein, conserved	-0.63	-0.50	-0.57	0.09	-	-	-	-		
TK1424	Hypothetical protein, conserved_COG2407	0.41	-0.01	0.20	0.30	1.15	0.39	0.77	0.53		
TK1425	Hypothetical protein, conserved_COG1458	-0.59	-0.20	-0.40	0.28	1.29	1.25	1.27	0.03		
TK1426	Ribose 5-phosphate isomerase_COG0120	-0.16	-0.04	-0.10	0.08	-0.73	-1.51	-1.12	0.55		
TK1427	Hypothetical membrane protein, conserved	-0.18	-0.25	-0.21	0.05	-0.27	0.16	-0.06	0.30		
TK1428	Cleavage and polyadenylation specficity factor	-0.44	-0.28	-0.36	0.11	0.47	-0.23	0.12	0.49		
TK1429	Proteasome, beta subunit_COG0638	0.34	0.01	0.18	0.23	-0.48	-0.22	-0.35	0.18		
TK1430	Hypothetical protein	0.33	0.18	0.25	0.11	-0.20	-0.21	-0.21	0.01	coding	
TK1431	Glutamate dehydrogenase_COG0334	0.03	-0.58	-0.27	0.43	-1.28	-1.21	-1.24	0.05	coding	coding
TK1432	Sodium-dependent transporter, SNF family_CO	-0.36	-0.45	-0.40	0.07	-	-1.32	-	-		
TK1433	Hypothetical protein, conserved	-	-0.27	-	-	-	-	-	-		
TK1434	alpha-Glucosidase	-0.59	-0.44	-0.52	0.10	-0.63	-0.89	-0.76	0.18		
TK1435	Nitrogen regulatory protein P-II_COG0347	0.32	0.16	0.24	0.12	-	-	-	-		
TK1436	Archaeal branching enzyme_COG1543	0.38	0.03	0.21	0.24	-	-0.78	-	-	coding	
TK1437	Hypothetical membrane protein	-0.05	-0.28	-0.17	0.16	-	2.17	-	-		
TK1438	Predicted fibronectin-binding protein_COG1293	0.14	0.14	0.14	0.00	0.27	-0.16	0.05	0.31		
TK1439	Probable nickel responsive regulator_COG0864	0.25	-0.05	0.10	0.21	0.25	0.46	0.35	0.15		
TK1440	Hypothetical protein, conserved	-0.94	-0.57	-0.76	0.26	0.81	0.10	0.46	0.50		
TK1441	Hypothetical protein	-0.70	-0.86	-0.78	0.11	-0.62	-0.74	-0.68	0.09		
TK1442	Tryptophan synthase beta subunit-related prot	0.12	-0.27	-0.07	0.27	-	-	-	-		
TK1443	Aspartate-semialdehyde dehydrogenase_COG0	0.10	-0.09	0.00	0.14	1.20	-	-	-	coding	
TK1444	Homoserine kinase_COG0083	-	-0.37	-	-	-	-	-	-	coding	
TK1445	Aspartokinase_COG0527	-0.19	0.14	-0.03	0.23	-	-	-	-	coding	
TK1446	Methionine synthase II (cobalamin-independent	0.62	0.21	0.41	0.29	2.53	0.20	1.36	1.65	coding	
TK1447	Methionine synthase II (cobalamin-independent	-0.34	-0.24	-0.29	0.07	0.92	6.76	3.84	4.13		
TK1448	5,10-Methylenetetrahydrofolate reductase_CO	-0.51	-	-	-	-	1.56	-	-		
TK1449	Cystathionine gamma-synthase_COG0626	0.40	0.12	0.26	0.20	-	-	-	-		
TK1450	Ribonuclease P component, Rpp30 homolog_C	0.37	0.38	0.37	0.00	-	-	-	-		

TK1451	Predicted exosome subunit, DUF54 family_COG	1.32	1.29	1.30	0.02	2.01	2.24	2.12	0.16	coding	coding
TK1452	ABC-type multidrug transport system, ATPase	2.89	2.72	2.80	0.12	1.26	2.18	1.72	0.65	5' (-103)	
TK1453	Hypothetical protein, conserved	3.14	3.75	3.45	0.44	-	-	-	-	5' (-98)	
TK1454	LSU ribosomal protein L15E_COG1632	0.11	0.10	0.11	0.00	-1.11	-0.87	-0.99	0.17		
TK1455	Xaa-Pro aminopeptidase_COG0006	0.08	-0.08	0.00	0.11	-	-	-	-	coding	
TK1456	Probable phosphate transport system regulator	0.02	-0.14	-0.06	0.11	-1.22	-0.87	-1.04	0.24		
TK1457	Probable phosphate transport system regulator	-0.42	-0.35	-0.38	0.05	-0.19	-0.24	-0.21	0.04		
TK1458	Magnesium transporter_COG1824	-0.07	-0.13	-0.10	0.04	-0.87	-2.29	-1.58	1.00	coding	
TK1459	Hypothetical protein, conserved	-0.28	-0.55	-0.42	0.19	-1.18	-0.79	-0.99	0.27		
TK1460	Predicted endonuclease-methyltransferase fus	-0.68	-0.91	-0.80	0.16	-0.81	0.13	-0.34	0.66		
TK1461	leucyl-tRNA synthetase_COG0495	0.37	0.51	0.44	0.10	-1.40	-0.58	-0.99	0.58	coding	
TK1462	Hypothetical membrane protein	2.74	2.86	2.80	0.09	0.76	0.42	0.59	0.24		
TK1463	Hypothetical protein, conserved	6.38	6.29	6.33	0.06	0.68	0.47	0.58	0.15	5' (-98)	
TK1464	Hypothetical protein, conserved	0.42	0.36	0.39	0.04	-	-0.33	-	-		
TK1465	Archaeal ATPase, fused to C-terminal DUF234	-0.69	-0.21	-0.45	0.34	0.48	2.22	1.35	1.23		
TK1466	ArgE/DapE-related deacylase_COG0624	-0.76	-0.13	-0.44	0.45	0.60	0.47	0.54	0.09		
TK1467	Predicted membrane-associated metallopeptid	0.08	0.12	0.10	0.03	-0.25	-0.47	-0.36	0.16		5' (+40)
TK1468	Bifunctional short-chain isoprenyl diphosphate	-0.15	-0.09	-0.12	0.04	-0.82	-1.22	-1.02	0.28	coding	
TK1469	Hydrolase, metallo-beta-lactamase superfamily	-0.46	-0.11	-0.29	0.25	1.30	1.14	1.22	0.12	coding	
TK1470	Isopentenyl-diphosphate delta-isomerase_COG	0.54	0.19	0.37	0.25	-1.07	-0.85	-0.96	0.15	coding	
TK1471	Aspartate racemase_COG1794	-0.42	-0.13	-0.28	0.20	-	-1.52	-	-		
TK1472	CinA-related molybdopterin-binding protein_CO	0.13	0.10	0.11	0.03	1.01	0.48	0.74	0.38		
TK1473	Amino acid kinase_COG1608	0.72	0.35	0.54	0.27	-0.73	0.08	-0.33	0.57		
TK1474	Mevalonate kinase_COG1577	-0.37	-0.27	-0.32	0.07	-0.10	-0.40	-0.25	0.22		
TK1475	Hypothetical protein, conserved, DUF86 family_	-1.05	-0.43	-0.74	0.43	-	-	-	-		
TK1476	Nucleotidyltransferase_COG1708	-0.53	-0.30	-0.42	0.16	-	-0.96	-	-		
TK1477	Hypothetical protein, conserved, DUF52 family_	-0.02	-0.17	-0.09	0.11	-	0.03	-	-	coding	
TK1478	Threonine synthase_COG0498	-0.20	-0.10	-0.15	0.07	2.92	0.45	1.68	1.74		
TK1479	Uridine phosphorylase_COG2820	0.39	0.20	0.29	0.13	-0.48	-0.33	-0.41	0.10		
TK1480	Hypothetical protein, conserved	0.43	0.28	0.35	0.11	1.22	-0.49	0.36	1.21		
TK1481	NADH:polysulfide oxidoreductase_COG0446	-0.35	-0.26	-0.30	0.07	-0.83	-0.83	-0.83	0.00		
TK1482	Purine-nucleoside phosphorylase_COG0005	-0.75	-0.49	-0.62	0.18	-0.65	-0.29	-0.47	0.25		
TK1483	Hypothetical protein, conserved	-0.01	0.05	0.02	0.04	-	2.29	-	-		coding
TK1484	Hypothetical protein, conserved	2.13	1.68	1.91	0.31	0.20	0.98	0.59	0.55		
TK1485	Hypothetical protein	-0.29	-0.43	-0.36	0.10	0.16	0.15	0.15	0.01		
TK1486	Signal recognition particle, SRP54 subunit_COG	0.35	0.15	0.25	0.14	-0.47	-0.85	-0.66	0.27		
TK1487	Predicted transcription regulator, Lrp/AsnC fa	-0.13	-0.08	-0.10	0.04	1.75	-0.36	0.70	1.49		
TK1488	Hypothetical protein, conserved, UPF0153 fami	0.44	0.15	0.30	0.21	-	-1.36	-	-		
TK1489	Adenine phosphoribosyltransferase, fused to N	-0.58	-0.12	-0.35	0.32	-	0.09	-	-		
TK1490	Hypothetical protein	-0.43	-0.17	-0.30	0.19	-	-1.15	-	-		
TK1491	Transcription regulator, Lrp/AsnC family_COG1	-0.17	-0.16	-0.17	0.00	-1.34	-0.34	-0.84	0.71		
TK1492	Hypothetical protein, conserved_COG0639	0.19	0.14	0.16	0.04	-	-1.06	-	-		
TK1493	Hypothetical protein, conserved, FUN14 family_	-0.30	-0.18	-0.24	0.08	0.05	0.07	0.06	0.01		
TK1494	Transcription regulator, PadR-like family_COG1	-1.09	-0.45	-0.77	0.45	-1.47	-0.82	-1.15	0.46		
TK1495	LSU ribosomal protein L40E_COG1552	0.76	0.42	0.59	0.24	0.54	0.40	0.47	0.10		
TK1496	SSU ribosomal protein S2P_COG0052	0.32	0.23	0.27	0.07	-0.53	-0.71	-0.62	0.13		
TK1497	Enolase-related protein_COG0148	-0.34	-0.12	-0.23	0.16	-	-	-	-		
TK1498	DNA-directed RNA polymerase, subunit K_COG	0.86	0.39	0.63	0.33	-	-1.18	-	-		
TK1499	DNA-directed RNA polymerase subunit N_COG	0.14	0.24	0.19	0.07	-	0.18	-	-		
TK1500	SSU ribosomal protein S9P_COG0103	-0.28	0.03	-0.13	0.23	-0.92	-1.04	-0.98	0.09		
TK1501	LSU ribosomal protein L13P_COG0102	0.36	0.30	0.33	0.04	-1.46	-1.36	-1.41	0.07		
TK1502	LSU ribosomal protein L18E_COG1727	0.49	0.27	0.38	0.15	-1.07	-1.40	-1.23	0.23		
TK1503	DNA-directed RNA polymerase, subunit D_COG	-0.12	0.04	-0.04	0.11	-1.23	-1.16	-1.20	0.05		
TK1504	SSU ribosomal protein S11P_COG0100	0.12	0.01	0.07	0.08	-1.65	-1.20	-1.42	0.32		
TK1505	SSU ribosomal protein S4P_COG0522	0.36	0.24	0.30	0.09	-1.33	-1.33	-1.33	0.00	coding	
TK1506	SSU ribosomal protein S13P_COG0099	0.59	0.28	0.43	0.22	-	-1.12	-	-		
TK1507	Ribosomal RNA small subunit methyltransferas	0.57	0.38	0.47	0.13	0.54	-0.66	-0.06	0.85		
TK1508	Hypothetical membrane protein, conserved	-0.06	0.01	-0.02	0.05	-0.48	-0.22	-0.35	0.19		
TK1509	tRNA pseudouridine synthase B_COG0130	-0.43	-0.52	-0.47	0.06	-	-0.96	-	-		
TK1510	Hypothetical protein, conserved	-1.45	-0.86	-1.16	0.42	-	1.25	-	-		
TK1511	Hypothetical protein, conserved, UPF0150 fami	-0.90	-0.87	-0.88	0.02	-	0.63	-	-		
TK1512	Short-chain alcohol dehydrogenase_COG0300	-0.42	-0.54	-0.48	0.09	-0.76	-1.65	-1.20	0.63		
TK1513	LSU ribosomal protein L14E_COG2163	0.81	0.52	0.66	0.21	-0.01	-1.59	-0.80	1.12		
TK1514	Cytidylate kinase_COG1102	0.32	0.40	0.36	0.06	-1.17	-1.86	-1.51	0.49		
TK1515	LSU ribosomal protein L34E_COG2174	-0.16	-0.02	-0.09	0.09	-0.80	-1.04	-0.92	0.17		
TK1516	Hypothetical membrane protein, conserved, DU	0.08	0.02	0.05	0.05	0.36	0.17	0.26	0.14		
TK1517	Archaeal adenylate kinase_COG2019	-0.04	-0.04	-0.04	0.00	-0.65	0.03	-0.31	0.48		
TK1518	Preprotein translocase, SecY subunit_COG020	-0.38	-0.08	-0.23	0.21	-1.29	-1.43	-1.36	0.11		
TK1519	LSU ribosomal protein L15P_COG0200	0.29	0.35	0.32	0.04	-1.93	-2.37	-2.15	0.31		
TK1520	LSU ribosomal protein L30P_COG1841	0.42	0.46	0.44	0.03	-1.88	-1.79	-1.84	0.07		
TK1521	SSU ribosomal protein S5P_COG0098	0.98	0.72	0.85	0.19	-1.74	-1.67	-1.70	0.05	coding	
TK1522	LSU ribosomal protein L18P_COG0256	0.09	0.41	0.25	0.23	-	-1.66	-	-		
TK1523	LSU ribosomal protein L19E_COG2147	0.51	-0.02	0.25	0.37	-1.50	-1.64	-1.57	0.09		
TK1524	LSU ribosomal protein L32E_COG1717	0.86	0.58	0.72	0.20	-2.20	-1.95	-2.07	0.18		
TK1525	LSU ribosomal protein L6P_COG0097	0.47	0.46	0.46	0.01	-1.25	-1.55	-1.40	0.21		
TK1526	SSU ribosomal protein S8P_COG0096	0.73	0.53	0.63	0.14	-	-1.56	-	-		
TK1527	SSU ribosomal protein S14P_COG0199	1.27	0.79	1.03	0.34	-	-	-	-		
TK1528	LSU ribosomal protein L5P_COG0094	-0.06	0.42	0.18	0.34	-1.83	-1.48	-1.65	0.25		
TK1529	SSU ribosomal protein S4E_COG1471	0.88	0.56	0.72	0.23	2.17	-1.17	0.50	2.36		
TK1530	LSU ribosomal protein L24P_COG0198	-0.19	0.04	-0.07	0.17	-1.14	-1.51	-1.33	0.26		
TK1531	LSU ribosomal protein L14P_COG0093	0.85	0.58	0.71	0.19	-1.60	-1.65	-1.62	0.03	5' (+20)	
TK1532	SSU ribosomal protein S17P_COG0186	0.53	0.34	0.44	0.13	-1.50	-1.40	-1.45	0.07		
TK1533	Ribonuclease P component, Rpp29 homolog_CO	0.42	0.44	0.43	0.01	-	-1.13	-	-		
TK1534	Protein translation factor SUI1 homolog_COG0	-0.03	-0.12	-0.07	0.06	-1.90	-1.84	-1.87	0.04		
TK1535	LSU ribosomal protein L29P_COG0255	0.77	0.65	0.71	0.08	-0.28	-0.89	-0.58	0.43		
TK1536	SSU ribosomal protein S3P_COG0092	0.69	0.52	0.61	0.12	-	-1.58	-	-		
TK1537	LSU ribosomal protein L22P_COG0091	-0.39	-0.26	-0.32	0.09	-2.01	-2.23	-2.12	0.16		
TK1538	SSU ribosomal protein S19P_COG0185	-0.02	0.13	0.06	0.11	-1.49	-1.74	-1.62	0.18		
TK1539	LSU ribosomal protein L2P_COG0090	-0.58	-0.19	-0.39	0.28	-1.17	-1.58	-1.37	0.29	coding	
TK1540	LSU ribosomal protein L23P_COG0089	0.29	0.22	0.25	0.05	-1.42	-1.53	-1.47	0.08		
TK1541	LSU Ribosomal protein L4P_COG0088	0.05	0.08	0.06	0.02	-1.65	-1.84	-1.74	0.13		

TK1542	LSU ribosomal protein L3P_COG0087	0.49	0.36	0.43	0.09	-1.14	-1.09	-1.12	0.03	coding		
TK1543	Hypothetical protein, conserved, DUF171 family	0.44	0.06	0.25	0.27	-	-0.37	-	-			
TK1544	Archaeal ATPase, fused to C-terminal DUF234	-0.30	-0.36	-0.33	0.04	-0.41	-	-	-			
TK1545	Hypothetical protein, conserved, DUF135 family	-0.73	-0.79	-0.76	0.04	-0.61	-0.97	-0.79	0.25			
TK1546	LSU ribosomal protein L10E_COG0197	0.26	0.21	0.23	0.03	-1.39	-1.34	-1.36	0.04			
TK1547	Predicted permease, major facilitator superfam	-0.25	-0.35	-0.30	0.07	-	-0.37	-	-			
TK1548	Probable serine--glyoxylate aminotransferase,	0.10	0.00	0.05	0.06	-1.00	-1.60	-1.30	0.42			
TK1549	Predicetd ATPase_COG0630	0.27	0.05	0.16	0.15	-0.44	-0.50	-0.47	0.04			
TK1550	Asparaginyl-tRNA synthetase-related protein (	-1.20	-0.82	-1.01	0.27	-	-0.04	-	-			
TK1551	Predicted ATPase, PP-loop superfamily_COG0	-0.09	-0.33	-0.21	0.17	0.42	0.74	0.58	0.23			
TK1552	Hypothetical membrane protein, conserved_CO	-	-0.27	-	-	-	-	-	-			
TK1553	Hypothetical protein, conserved	-0.31	-0.22	-0.27	0.06	-0.48	0.30	-0.09	0.55			
TK1554	Glycosyltransferase, family 2_COG1215	-0.91	-0.58	-0.74	0.24	-0.63	-0.54	-0.59	0.07			
TK1555	Hypothetical membrane protein, conserved	-0.78	-0.48	-0.63	0.21	-	0.79	-	-			
TK1556	ATPase, PP-loop superfamily_COG0037	-0.25	-0.05	-0.15	0.14	-	0.56	-	-	5' (+7)		
TK1557	Predicted dehydrogenase_COG2509	-1.23	-1.08	-1.15	0.11	-0.33	-0.53	-0.43	0.14	coding		
TK1558	Hypothetical protein, conserved, containing CB	-0.37	-0.20	-0.29	0.12	-	-	-	-			
TK1559	NapA-type sodium/hydrogen antiporter_COG04	0.08	-0.01	0.03	0.07	-	2.07	-	-			
TK1560	NapA-type sodium/hydrogen antiporter_COG04	0.02	-0.16	-0.07	0.13	-	1.23	-	-			
TK1561	Hypothetical membrane protein, conserved, Ma	-0.08	-0.23	-0.15	0.10	-	-0.94	-	-			
TK1562	Histidyl-tRNA synthetase_COG0124	-0.36	-0.13	-0.25	0.16	0.28	0.76	0.52	0.34			
TK1563	Phospholipase D-related protein	-0.40	-0.27	-0.33	0.09	-	-0.69	-	-	coding		
TK1564	Hypothetical protein	-0.42	-0.19	-0.31	0.16	5.53	2.72	4.13	1.99			
TK1565	Hypothetical protein, conserved	0.65	0.54	0.60	0.08	-	0.32	-	-			
TK1566	Hypothetical protein, conserved	3.46	3.72	3.59	0.18	-0.52	1.57	0.52	1.48			
TK1567	Alanyl-tRNA synthetase_COG0013	-0.33	-0.29	-0.31	0.03	-0.88	-1.00	-0.94	0.08			
TK1568	Sodium/proline symporter, SSF family_COG059	-1.02	-0.40	-0.71	0.44	-	1.02	-	-			
TK1569	Iron-containing alcohol dehydrogenase_COG14	-0.58	-0.30	-0.44	0.20	2.29	1.53	1.91	0.54			
TK1570	Hypothetical protein	-0.82	-0.48	-0.65	0.24	-	-1.21	-	-			
TK1571	Hypothetical protein, conserved	-1.20	-0.94	-1.07	0.19	1.18	-0.60	0.29	1.26			
TK1572	NGG1p interacting factor 3 homolog_COG0327	0.18	-0.07	0.05	0.18	0.13	0.26	0.20	0.09			
TK1573	Archaeal ATPase, fused to C-terminal DUF234	0.02	-0.13	-0.05	0.10	-1.18	-	-	-			
TK1574	Histone acetyltransferase Elp3 homolog_COG1	-0.49	-0.51	-0.50	0.02	0.93	2.87	1.90	1.37	coding		
TK1575	Hypothetical membrane protein, conserved, co	0.23	0.20	0.21	0.02	1.01	0.22	0.62	0.56			
TK1576	Hypothetical membrane protein, conserved_CO	-0.42	0.11	-0.15	0.37	-	0.33	-	-			
TK1577	Hypothetical membrane protein, conserved_CO	2.50	2.58	2.54	0.06	-0.86	-0.38	-0.62	0.34	operon	operon	
TK1578	Hypothetical membrane protein, conserved_CO	4.01	3.41	3.71	0.42	-0.31	-0.27	-0.29	0.02	operon	operon	
TK1579	ABC-type multidrug transport system, ATPase	-	3.54	-	-	-0.18	-0.18	-0.18	0.01	5' (-30)	5' (-94)	
TK1580	Hypothetical protein, conserved, UPF0153 fami	0.76	0.20	0.48	0.39	-0.39	-0.35	-0.37	0.03	5' (-108)	5' (-44)	
TK1581	Hypothetical protein, conserved, UPF0113 fami	-0.05	0.16	0.06	0.15	5.16	-0.07	2.55	3.69			
TK1582	Hypothetical membrane protein	5.70	5.93	5.81	0.16	0.84	1.01	0.93	0.12	5' (-92)		
TK1583	Hypothetical protein	2.55	2.82	2.69	0.20	-	0.67	-	-	operon		
TK1584	Hypothetical membrane protein	2.54	2.70	2.62	0.11	-	-	-	-	operon		
TK1585	Hypothetical protein	2.62	2.48	2.55	0.09	4.34	-0.17	2.09	3.19	operon		
TK1586	Hypothetical membrane protein, conserved	2.03	2.10	2.07	0.05	-	4.47	-	-			
TK1587	Hypothetical membrane protein	1.42	1.66	1.54	0.17	1.89	1.28	1.59	0.43			
TK1588	ABC-type multidrug transport system, ATPase	1.85	1.88	1.87	0.02	-	2.44	-	-			
TK1589	S-layer-like array protein	2.33	2.69	2.51	0.25	0.19	-0.26	-0.04	0.31			
TK1590	Predicted ATPase, AAA superfamily_COG0467	1.49	1.46	1.48	0.02	0.74	0.53	0.64	0.15	5' (-2)	5' (-20)	
TK1591	Predicted transcription regulator, encoded nex	1.09	1.56	1.33	0.33	1.89	0.36	1.13	1.09	operon	operon	
TK1592	S-Adenosylmethionine decarboxylase proenzyr	0.71	0.53	0.62	0.13	-	-0.65	-	-			
TK1593	Protein-export membrane protein SecF_COG0	-0.24	-0.23	-0.23	0.01	-0.03	0.07	0.02	0.07			
TK1594	Protein-export membrane protein SecD_COG0	-0.60	-0.88	-0.74	0.20	-0.48	-0.79	-0.64	0.22			
TK1595	Trk-type pottasium transport system, NAD-bir	-0.42	-0.31	-0.37	0.07	-1.54	-1.01	-1.27	0.37			
TK1596	Archaeal/vacuolar-type H+-ATPase, subunit H	-0.30	-0.17	-0.23	0.09	-0.87	-0.74	-0.81	0.09			
TK1597	Archaeal/vacuolar-type H+-ATPase, subunit I	0.31	0.12	0.22	0.14	-0.85	-0.30	-0.58	0.39			
TK1598	Archaeal/vacuolar-type H+-ATPase, subunit K	-0.20	-0.18	-0.19	0.01	-1.68	-1.76	-1.72	0.06			
TK1599	Archaeal/vacuolar-type H+-ATPase, subunit E	-0.73	-0.30	-0.51	0.30	-1.04	-0.62	-0.83	0.30			
TK1600	Archaeal/vacuolar-type H+-ATPase, subunit C	-0.04	-0.03	-0.03	0.01	-	-0.72	-	-			
TK1601	Archaeal/vacuolar-type H+-ATPase, subunit F	0.33	0.06	0.19	0.19	-	-0.43	-	-			
TK1602	Archaeal/vacuolar-type H+-ATPase, subunit A	0.45	0.10	0.28	0.25	-0.97	-0.90	-0.94	0.05	coding		
TK1603	Archaeal/vacuolar-type H+-ATPase, subunit B	0.18	-0.01	0.09	0.13	-1.35	-1.24	-1.29	0.08	coding		
TK1604	Archaeal/vacuolar-type H+-ATPase, subunit D	0.12	-0.15	-0.01	0.19	-1.09	-1.01	-1.05	0.06			
TK1605	Hydrolase, metallo-beta-lactamase superfamily	0.23	0.04	0.13	0.14	1.94	-0.33	0.81	1.60			
TK1606	Methyl-accepting chemotaxis protein_COG084	-0.32	-0.28	-0.30	0.02	-	-	-	-	coding		
TK1607	Alanyl-tRNA synthetase-related protein (C-te	-0.64	-0.26	-0.45	0.27	1.93	2.17	2.05	0.17			
TK1608	Hypothetical protein, conserved, DUF257 family	-0.25	-0.17	-0.21	0.05	-0.59	-0.14	-0.36	0.32			
TK1609	Hypothetical protein, conserved, DUF257 family	0.68	0.33	0.50	0.25	0.95	1.24	1.10	0.20			
TK1610	Hypothetical protein, conserved	-0.28	-0.14	-0.21	0.09	-0.19	-0.04	-0.12	0.10			
TK1611	Predicted metal-dependent hydrolase_COG183	-0.10	-0.11	-0.11	0.01	-	-	-	-			
TK1612	Glutamate synthase beta chain-related oxidore	-	-0.49	-	-	-	-1.43	-	-			
TK1613	NADH:ubiquinone oxidoreductase, NADH-bindi	-0.80	-0.43	-0.61	0.26	-0.88	-1.29	-1.08	0.29			
TK1614	NADH:ubiquinone oxidoreductase, subunit E_C	-0.07	-0.50	-0.29	0.30	-0.33	0.11	-0.11	0.31	coding		
TK1615	RNA 3'-terminal phosphate cyclase_COG0430	-0.51	-0.33	-0.42	0.13	0.27	-0.50	-0.11	0.54	coding		
TK1616	Hypothetical protein	-0.30	-0.18	-0.24	0.08	-	-	-	-			
TK1617	Hypothetical protein, conserved	-0.48	-0.51	-0.49	0.03	-0.96	-0.99	-0.97	0.02			
TK1618	Metallophosphoesterase, calcineurin superfami	0.15	0.11	0.13	0.03	0.03	0.24	0.13	0.15			
TK1619	Hypothetical protein, conserved, DUF1288 fam	-0.45	-0.19	-0.32	0.19	-	0.40	-	-			
TK1620	DNA replication licensing factor, MCM2/3/5 fa	-0.34	-0.06	-0.20	0.20	-1.01	-0.90	-0.95	0.08			
TK1621	Translation initiation factor eIF-2, beta subunit	0.08	-0.24	-0.08	0.23	-1.30	-1.10	-1.20	0.14			
TK1622	Methylmalonyl-CoA decarboxylase, alpha subu	0.58	0.27	0.42	0.22	-0.92	-0.46	-0.69	0.33	coding		
TK1623	Methylmalonyl-CoA decarboxylase, delta subun	0.10	0.04	0.07	0.04	-0.75	-0.95	-0.85	0.14			
TK1624	Methylmalonyl-CoA decarboxylase, gamma sub	-0.93	-0.26	-0.59	0.48	-1.50	-1.44	-1.47	0.04			
TK1625	Methylmalonyl-CoA decarboxylase, beta subun	-0.05	-0.05	-0.05	0.00	-1.45	-1.41	-1.43	0.03			
TK1626	Hypothetical protein, conserved, containing CB	0.34	0.29	0.31	0.04	-0.59	-1.14	-0.86	0.39			
TK1627	Homoserine dehydrogenase_COG0460	-0.10	-0.05	-0.07	0.04	0.46	0.89	0.67	0.30			
TK1628	Hypothetical protein	-0.18	-0.08	-0.13	0.07	-	0.97	-	-			
TK1629	Hypothetical protein, conserved	-0.43	0.00	-0.21	0.31	-	-0.44	-	-			
TK1630	Hypothetical protein, conserved, containing ZP	-0.61	-0.17	-0.39	0.31	-0.14	1.18	0.52	0.93			
TK1631	Hypothetical protein, conserved_COG2450	-0.19	-0.09	-0.14	0.07	0.36	-0.35	0.00	0.50			
TK1632	Hypothetical membrane protein	-0.03	-0.24	-0.14	0.15	-	0.22	-	-			

TK1633	Exosome subunit Rrp42p homolog, 3'-5' exorib	0.13	-0.02	0.05	0.11	-1.55	-1.06	-1.31	0.35		
TK1634	Exosome subunit Rrp41p homolog, 3'-5' exorib	-0.96	-0.48	-0.72	0.34	-0.91	-0.49	-0.70	0.30		
TK1635	Exosome subunit Rrp4p homolog, RNA-binding	-0.35	-0.36	-0.36	0.00	-1.46	-0.82	-1.14	0.46		
TK1636	Predicted exosome subunit, UPF0023 family_C	-0.38	-0.29	-0.33	0.06	-1.06	-0.72	-0.89	0.24	coding	
TK1637	Proteasome, alpha subunit_COG0638	-0.83	-0.42	-0.62	0.29	-1.13	-1.25	-1.19	0.09		
TK1638	Hypothetical membrane protein	-	-0.29	-	-	-	-	-	-		
TK1639	Probable bis(5'-adenosyl)-triphosphatase, HIT	-0.10	-0.12	-0.11	0.01	0.05	0.24	0.14	0.14		
TK1640	Nucleotide pyrophosphohydrolase_COG1694	-0.62	-0.50	-0.56	0.09	1.25	0.36	0.80	0.63		
TK1641	Hypothetical protein, conserved	-0.78	-0.77	-0.78	0.01	-0.64	-0.54	-0.59	0.07		
TK1642	Hypothetical membrane protein, conserved	-0.41	-0.68	-0.55	0.19	-	-0.27	-	-		
TK1643	Indolepyruvate: ferredoxin oxidoreductase, alph	-0.21	-0.31	-0.26	0.07	-1.24	-1.05	-1.15	0.14		
TK1644	Predicted nucleic acid-binding protein, contain	0.21	-0.15	0.03	0.26	-0.09	0.81	0.36	0.64		
TK1645	Hypothetical protein	0.14	-0.13	0.01	0.19	-	-	-	-		
TK1646	Hypothetical protein, conserved	-0.38	-0.31	-0.34	0.05	-	-1.20	-	-		
TK1647	Hypothetical protein	-0.60	-0.62	-0.61	0.01	-	-0.90	-	-		
TK1648	Hypothetical protein	-0.11	-0.26	-0.18	0.10	-	0.49	-	-		
TK1649	Hypothetical membrane protein, conserved, DU	-0.42	-0.38	-0.40	0.03	-	-0.76	-	-	coding	
TK1650	Probable nicotinamidase_COG1335	-0.02	-0.28	-0.15	0.19	-0.49	-0.48	-0.49	0.00		
TK1651	Hypothetical protein, conserved_COG2886	0.25	-0.29	-0.02	0.38	0.14	-0.10	0.02	0.17		
TK1652	Predicted thioesterase_COG2050	-0.77	-0.48	-0.62	0.21	-0.91	-1.36	-1.14	0.32		
TK1653	Hypothetical membrane protein, conserved	-0.04	0.16	0.06	0.14	0.96	1.73	1.34	0.54		
TK1654	Transcription regulator, PadR-like family_COG1	-0.14	-0.10	-0.12	0.02	-	-	-	-		
TK1655	Predcited permease, major facilitator superfam	-0.19	-0.27	-0.23	0.06	-	-	-	-		
TK1656	L-Asparaginase_COG0252	-0.32	-0.07	-0.19	0.18	-	-	-	-		
TK1657	Hypothetical protein, conserved	-0.32	-0.20	-0.26	0.09	-	-	-	-		
TK1658	Hypothetical protein, conserved	-0.54	-0.37	-0.45	0.12	-	2.31	-	-		
TK1659	Small neutral amino acid transporter_COG2095	-0.13	0.01	-0.06	0.09	-	-0.96	-	-	5' (-27)	
TK1660	Hypothetical protein, conserved	5.40	4.85	5.12	0.39	-	3.16	-	-	5' (-87)	
TK1661	Hypothetical membrane protein, conserved_CO	2.84	3.18	3.01	0.24	-	2.21	-	-		
TK1662	Hypothetical protein, conserved, internal deleti	0.21	0.11	0.16	0.07	-	-	-	-		
TK1663	Hypothetical protein, conserved, insertion	-0.02	-0.15	-0.08	0.09	-	-0.06	-	-	coding	
TK1664	Hypothetical protein, conserved, insertion	-0.04	-0.15	-0.10	0.08	-0.20	-0.39	-0.30	0.13		
TK1665	Hypothetical protein, conserved	0.04	-0.06	-0.01	0.07	0.11	-1.01	-0.45	0.79		
TK1666	Hypothetical protein, conserved	-0.84	-0.72	-0.78	0.09	-	-1.50	-	-		
TK1667	Hypothetical membrane protein, conserved, co	-	-0.72	-	-	-0.86	-1.09	-0.98	0.16		
TK1668	Hypothetical protein, conserved	-1.05	-0.77	-0.91	0.20	-	0.04	-	-		
TK1669	Cell division GTPase_COG0206	-0.56	-0.39	-0.48	0.11	-	0.20	-	-		
TK1670	Hypothetical protein, conserved	0.05	-0.12	-0.03	0.12	-	0.19	-	-		
TK1671	Hypothetical protein, conserved, radical SAM s	-0.01	0.51	0.25	0.37	-	-0.45	-	-		
TK1672	Hypothetical protein	0.36	0.07	0.21	0.21	-	2.46	-	-		
TK1673	N5-Glutamine methyltransferase, HemK family_	-0.39	-0.36	-0.37	0.02	-	4.09	-	-		
TK1674	Flavin reductase-related oxidoreductase_COG1	-0.15	-0.15	-0.15	0.00	-	-0.26	-	-		
TK1675	Subtilisin-like serine protease precursor_COG1	-0.12	-0.51	-0.31	0.28	-	3.78	-	-	coding	
TK1676	Nicotinate-nucleotide pyrophosphorylase_COG	-0.22	-0.53	-0.37	0.21	-0.35	-0.19	-0.27	0.11		
TK1677	Short-chain alcohol dehydrogenase_COG1028	-1.11	-	-	-	-0.23	-0.82	-0.53	0.42		
TK1678	Hypothetical membrane protein	2.74	3.07	2.90	0.23	0.71	0.47	0.59	0.17	coding	
TK1679	Hypothetical protein, conserved	6.36	6.10	6.23	0.19	1.91	2.61	2.26	0.49		
TK1680	Hypothetical protein	5.40	5.65	5.53	0.18	-	1.49	-	-	5' (-32)	
TK1681	Predicted hydrolase, metallo-beta-lactamase s	0.30	0.05	0.17	0.17	-	-	-	-		
TK1682	Hypothetical protein	-0.32	-0.39	-0.35	0.05	-	-	-	-		
TK1683	Hypothetical protein, conserved	-0.49	-0.22	-0.36	0.20	-	0.73	-	-		
TK1684	Ferredoxin:NADP oxidoreductase, alpha subuni	0.06	0.00	0.03	0.04	-1.42	-1.18	-1.30	0.17		
TK1685	Ferredoxin:NADP oxidoreductase, beta subunit	-0.53	-0.41	-0.47	0.09	0.06	0.61	0.34	0.39		
TK1686	Hypothetical protein, conserved, DUF137 famil	0.13	0.04	0.08	0.06	-0.15	-1.42	-0.79	0.90		
TK1687	Cysteine synthase_COG0031	-0.22	-0.32	-0.27	0.07	-0.81	-1.10	-0.95	0.21		
TK1688	Predicted transcription regulator, containing D	0.07	0.04	0.06	0.02	0.16	-	-	-		
TK1689	Subtilisin-like serine protease precursor_COG1	-0.03	-0.13	-0.08	0.07	-0.62	0.07	-0.28	0.49		
TK1690	Hypothetical membrane protein, conserved	-0.57	-0.19	-0.38	0.27	-	2.84	-	-		
TK1691	Hypothetical protein, conserved, DUF43 family_	-0.61	-0.09	-0.35	0.37	-0.98	-0.11	-0.55	0.61		
TK1692	Predicted ATPase, PP-loop superfamily_COG1	-0.74	-0.41	-0.57	0.24	4.51	1.02	2.77	2.47		
TK1693	Hypothetical protein, conserved, containing DU	-0.99	-0.81	-0.90	0.12	-0.22	1.97	0.88	1.55		
TK1694	Ferredoxin 1_COG1141	0.44	0.23	0.33	0.14	-	-	-	-		
TK1695	SSU ribosomal protein S27AE_COG1998	-0.32	-0.69	-0.50	0.26	0.07	-	-	-		
TK1696	SSU ribosomal protein S24E_COG2004	0.25	0.20	0.22	0.04	-0.30	-1.98	-1.14	1.19	coding	coding
TK1697	Hypothetical protein, conserved, DUF359 famil	0.39	0.10	0.25	0.20	-	-1.25	-	-		
TK1698	DNA-directed RNA polymerase subunit E''_CO	-	-0.17	-	-	-	-	-	-		
TK1699	DNA-directed RNA polymerase, subunit E'_CO	-0.92	-0.33	-0.63	0.41	-1.46	-1.46	-1.46	0.00		
TK1700	Inorganic pyrophosphatase_COG0221	-0.74	-0.38	-0.56	0.26	-1.82	-1.64	-1.73	0.12		
TK1701	Hypothetical protein, conserved	-	-0.72	-	-	-	-	-	-	coding	
TK1702	Hypothetical protein, conserved, DUF1102 fam	-0.66	-0.71	-0.69	0.03	2.46	-0.47	1.00	2.07	coding	coding
TK1703	Signal peptidase I, fused to C-terminal uncharа	-	-0.86	-	-	-	-1.12	-	-		coding
TK1704	Hypothetical protein, conserved	-0.70	-0.50	-0.60	0.14	0.48	-	-	-		
TK1705	Hypothetical protein, conserved	-0.58	-0.65	-0.61	0.05	1.73	-0.02	0.86	1.24		
TK1706	Hypothetical protein, conserved	-	-0.02	-	-	-	-	-	-		
TK1707	Hypothetical protein	-	0.21	-	-	-	-	-	-		
TK1708	UDP-glucose 4-epimerase_COG0451	0.35	0.40	0.38	0.04	0.00	2.07	1.03	1.46		
TK1709	Nucleotidyltransferase_COG1708	0.19	0.32	0.26	0.10	0.44	0.01	0.23	0.30		
TK1710	Hypothetical protein, conserved, DUF86 family_	-0.23	0.18	-0.02	0.29	-	-	-	-		
TK1711	Sugar-phosphate nucleotydyltransferase_COG1	0.33	0.32	0.33	0.01	-	-	-	-		coding
TK1712	Capsular polysaccharide biosynthesis protein_C	0.20	0.12	0.16	0.05	1.01	0.02	0.52	0.70		
TK1713	Glycosyltransferase, family 4	-	-	-	-	-	0.00	-	-		
TK1714	Glycosyltransferase, family 2_COG0463	-0.34	-0.28	-0.31	0.04	-	-0.59	-	-		
TK1715	CDP-glycerol:poly(glycerophosphate) glycerop	-0.58	-0.65	-0.62	0.05	-	-	-	-		
TK1716	Cytidylyltransferase_COG1211	-0.42	-0.33	-0.38	0.06	-	2.87	-	-		
TK1717	Glycosyltransferase, family 2_COG0463	-0.60	-0.34	-0.47	0.19	0.76	0.56	0.66	0.14		
TK1718	Oligosaccharyl transferase, STT3 subunit_COG	-0.93	-0.38	-0.66	0.39	-	-1.01	-	-		
TK1719	Capsular polysaccharide biosynthesis protein_C	-0.84	-0.69	-0.76	0.10	-	-1.43	-	-		
TK1720	Dolichol-phosphate mannosyltransferase_COG	-0.73	-0.73	-0.73	0.00	-	-	-	-		
TK1721	Glycosyltransferase, family 4_COG0438	-	-	-	-	-	-	-	-		
TK1722	Probable beta-1,3-galactosyltransferase_COG	-0.32	-0.25	-0.28	0.06	-	1.33	-	-		
TK1723	Glycosyltransferase, family 4_COG0438	0.40	0.61	0.50	0.15	2.32	-0.10	1.11	1.72	coding	

TK1724	Hypothetical protein, containing ATP/GTP-bin	-0.35	-0.30	-0.33	0.03	-	-1.72	-	-	coding	
TK1725	Hypothetical membrane protein, conserved	0.01	0.04	0.03	0.02	-0.59	-0.07	-0.33	0.37		
TK1726	Hypothetical protein, conserved, flame shift	-0.58	-0.43	-0.50	0.10	-1.62	-	-	-		
TK1727	Hypothetical protein, conserved, flame shift	-0.69	-0.58	-0.63	0.08	-	-	-	-		
TK1728	Hypothetical membrane protein, conserved	-0.26	-0.32	-0.29	0.04	-	0.12	-	-		
TK1729	Hypothetical membrane protein, conserved	-0.13	-0.16	-0.15	0.02	3.53	0.90	2.21	1.86		
TK1730	Hypothetical membrane protein	-	-0.17	-	-	-	-	-	-		
TK1731	Glycosyltransferase, family 4_COG0438	-	-0.59	-	-	-	-	-	-		
TK1732	Dolichol-phosphate mannosyltransferase, fused	0.42	-0.62	-0.10	0.74	-	-	-	-		
TK1733	Glycosyltransferase, family 1_COG0438	-0.74	-0.67	-0.71	0.05	-0.68	-	-	-		
TK1734	Predicted sugar phosphatase, HAD superfamily	0.11	0.22	0.17	0.08	1.18	1.49	1.33	0.22		
TK1735	Hypothetical protein, conserved	-	-0.59	-	-	-1.58	-0.92	-1.25	0.46		
TK1736	Ribonucleoside-diphosphate reductase; two int	-0.83	-0.40	-0.61	0.30	-1.10	-1.41	-1.25	0.22	coding	coding
TK1737	Xanthine/guanine phosphoribosyltransferase_C	0.23	-0.11	0.06	0.25	-1.28	-1.30	-1.29	0.01		
TK1738	2'-5' RNA ligase_COG1514	0.56	0.27	0.42	0.20	0.06	-0.36	-0.15	0.30		
TK1739	Hypothetical protein	3.21	3.38	3.29	0.12	1.78	3.90	2.84	1.50	5' (-32)	
TK1740	Hypothetical membrane protein, conserved	1.61	2.12	1.86	0.36	1.50	0.63	1.06	0.61	operon	
TK1741	tRNA nucleotidyltransferase (CCA-adding enzy	-0.24	-0.11	-0.18	0.10	-	-0.54	-	-		coding
TK1742	Hypothetical protein	-	0.02	-	-	-	-	-	-		
TK1743	Hypothetical protein, conserved	-0.46	-0.34	-0.40	0.08	0.89	-	-	-	coding	
TK1744	Hypothetical protein, conserved	-0.52	-0.57	-0.54	0.04	-1.46	-1.04	-1.25	0.30		
TK1745	Permease, drug/metabolite transporter (DMT)	-1.04	-0.74	-0.89	0.21	-1.13	-	-	-		
TK1746	Hypothetical protein, conserved	-	-0.54	-	-	-	-	-	-		
TK1747	Hypothetical protein, conserved, DUF84 family	-0.17	-0.19	-0.18	0.02	-	1.74	-	-		
TK1748	Isoleucyl-tRNA synthetase_COG0060	0.60	0.25	0.42	0.25	0.33	-0.13	0.10	0.32	coding	
TK1749	Hypothetical protein	1.40	1.21	1.31	0.13	-	1.75	-	-		
TK1750	Hypothetical protein, conserved	3.86	3.38	3.62	0.34	-	0.38	-	-	5' (+14)	
TK1751	Predicted nucleic acid-binding protein, contain	0.87	0.51	0.69	0.26	3.15	-0.79	1.18	2.79		
TK1752	Hypothetical protein, conserved, DUF217 famil	0.06	0.04	0.05	0.01	-	-	-	-		
TK1753	Hypothetical membrane protein, conserved	-0.10	-0.01	-0.06	0.06	-0.57	-0.79	-0.68	0.16		
TK1754	exo-beta-D-glucosaminidase_COG1874	-0.53	-0.29	-0.41	0.17	1.94	-	-	-		
TK1755	Archaeal glucosamine-6-phosphate deaminase	-0.38	-0.32	-0.35	0.04	-	-	-	-		
TK1756	ABC-type dipeptide/oligopeptide transport sys	-0.34	-0.46	-0.40	0.08	0.81	-0.40	0.20	0.86		
TK1757	ABC-type dipeptide/oligopeptide transport sys	-0.76	-0.41	-0.58	0.25	-	0.74	-	-		
TK1758	ABC-type dipeptide/oligopeptide transport sys	-0.47	-0.28	-0.38	0.13	0.43	1.14	0.79	0.50	coding	
TK1759	ABC-type dipeptide/oligopeptide transport sys	-0.62	-0.27	-0.44	0.25	3.49	-	-	-		
TK1760	ABC-type dipeptide/oligopeptide transport sys	-0.94	-	-	-	-	-	-	-	coding	
TK1761	beta-Glycosidase, GH1 family_COG2723	-0.22	-0.19	-0.21	0.02	-0.09	-0.37	-0.23	0.20		
TK1762	Hypothetical protein, conserved	0.45	0.13	0.29	0.23	-	1.72	-	-		
TK1763	Predicted nucleic acid-binding protein, contain	0.14	0.07	0.10	0.05	-	-1.12	-	-		
TK1764	N-Acetylchitobiose deacetylase_COG2120	0.66	0.02	0.34	0.45	4.06	0.83	2.44	2.28		
TK1765	Chitinase, containing dual catalytic domains_CO	0.00	-0.14	-0.07	0.10	0.32	1.51	0.92	0.84	coding	
TK1766	Hypothetical protein, conserved, radical SAM s	0.11	0.21	0.16	0.07	-1.09	-0.66	-0.88	0.31		
TK1767	Ribonuclease P component, Rpp14 homolog_CO	-0.71	-0.40	-0.55	0.22	-1.15	-0.25	-0.70	0.64		
TK1768	Glycogen synthase_COG0297	-0.41	-0.45	-0.43	0.03	-	-	-	-	coding	
TK1769	Predicted transcription regulator, DUF118 helix	0.28	0.18	0.23	0.07	-0.93	-0.73	-0.83	0.14		
TK1770	Cyclomaltodextrinase_COG0366	-0.27	-0.16	-0.21	0.08	-	1.24	-	-		coding
TK1771	ABC-type maltodextrin transport system, malt	-0.52	-0.77	-0.65	0.17	0.62	-0.12	0.25	0.52		
TK1772	ABC-type maltodextrin transport system, perm	-0.90	-0.93	-0.91	0.02	-	-0.45	-	-		
TK1773	ABC-type maltodextrin transport system, perm	-1.09	-1.07	-1.08	0.01	-	-	-	-		
TK1774	Amylopullulanase, GH57 family_COG1449;COG4	-0.61	-0.82	-0.72	0.14	1.52	1.52	1.52	0.00	coding	coding
TK1775	ABC-type maltdextrin transport system, ATPa	-0.60	-0.62	-0.61	0.01	-0.47	-0.03	-0.25	0.31		
TK1776	Hypothetical protein, conserved, UPF0146 fami	-0.44	-0.57	-0.51	0.09	-	3.01	-	-		
TK1777	Phosphopentomutase_COG1109	0.00	-0.23	-0.12	0.16	-0.09	-0.61	-0.35	0.37	coding	
TK1778	Predicted hydrolase, metallo-beta-lactamase s	0.18	-0.07	0.06	0.18	-0.41	0.17	-0.12	0.41		
TK1779	Oligopeptide transporter, OPT family_COG1297	-	-1.39	-	-	-	-1.21	-	-		coding
TK1780	Hypothetical protein, conserved	-1.38	-1.36	-1.37	0.01	-2.96	-0.96	-1.96	1.41		
TK1781	ArgE/DapE-related deacylase_COG0624	-0.31	-0.26	-0.29	0.04	0.02	0.00	0.01	0.01		
TK1782	Serine protease inhibitor Serpin homolog_COG4	0.71	0.66	0.68	0.04	0.09	0.30	0.19	0.15	5' (+22)	
TK1783	Hypothetical membrane protein	1.07	1.07	1.07	0.00	-0.01	0.12	0.06	0.09	5' (-83)	
TK1784	Predicted SAM-dependent methyltransferase,	-0.19	-0.11	-0.15	0.06	-0.21	-	-	-	5' (-110)	coding
TK1785	Probable tRNA/rRNA methyltransferase_COG1	-0.46	-0.33	-0.40	0.09	-1.28	-0.66	-0.97	0.44		
TK1786	Hypothetical protein, conserved	-0.72	-0.78	-0.75	0.05	-	-	-	-		
TK1787	Hypothetical membrane protein, conserved, DU	1.50	1.50	1.50	0.00	-	2.13	-	-	operon	
TK1788	Hypothetical protein, conserved	1.69	2.01	1.85	0.23	-	-	-	-	5' (-107)	
TK1789	ATPase, RecA superfamily_COG0467	-0.30	-0.13	-0.21	0.12	-0.43	-0.84	-0.64	0.29		
TK1790	Eukaryotic-type DNA primase, large subunit_C	-0.87	-0.35	-0.61	0.37	-1.24	-1.17	-1.20	0.05		
TK1791	Eukaryotic-type DNA primase, small subunit_C	0.30	0.29	0.30	0.01	1.64	-0.47	0.59	1.49		
TK1792	Permease, drug/metabolite transporter (DMT)	-0.80	-0.70	-0.75	0.07	-	-0.52	-	-		
TK1793	Hypothetical membrane protein, conserved	0.22	-0.25	-0.02	0.33	1.32	0.28	0.80	0.74	coding	
TK1794	Hypothetical membrane protein, conserved	-1.04	-0.40	-0.72	0.45	2.21	-	-	-		
TK1795	Hypothetical protein, conserved, DUF61 family	0.05	-0.04	0.01	0.06	1.11	0.39	0.75	0.51		
TK1796	Glutamine synthetase_COG0174	-2.16	-1.81	-1.98	0.25	-1.75	-1.71	-1.73	0.03		
TK1797	Permease, drug/metabolite transporter (DMT)	-1.34	-1.08	-1.21	0.19	-0.43	-0.16	-0.30	0.19		
TK1798	NH3-dependent NAD+ synthetase_COG0171	-0.67	-	-	-	-0.06	-1.37	-0.72	0.93		
TK1799	Hypothetical membrane protein, conserved	0.21	0.08	0.15	0.09	1.71	0.31	1.01	1.00		
TK1800	ABC-type dipeptide/oligopeptide transport sys	0.11	0.10	0.10	0.01	-1.80	-1.00	-1.40	0.57		
TK1801	ABC-type dipeptide/oligopeptide transport sys	-0.49	-0.13	-0.31	0.25	-1.75	-1.54	-1.65	0.15		
TK1802	ABC-type dipeptide/oligopeptide transport sys	-0.39	-0.30	-0.34	0.06	-	-1.60	-	-	coding	
TK1803	ABC-type dipeptide/oligopeptide transport sys	0.10	-0.04	0.03	0.10	-	0.04	-	-		
TK1804	ABC-type dipeptide/oligopeptide transport sys	0.18	0.25	0.21	0.04	-2.33	-2.65	-2.49	0.23	coding	coding
TK1805	Dihydroorotase_COG0044	0.40	0.29	0.35	0.08	-	-1.26	-	-		
TK1806	Probable dihydroorotate dehydrogenase, electr	0.09	0.04	0.06	0.03	-0.57	-0.03	-0.30	0.38	coding	coding
TK1807	Hypothetical protein, conserved, radical SAM s	-0.23	-0.14	-0.19	0.06	-	-0.67	-	-		
TK1808	Hypothetical membrane protein, conserved	-0.70	-0.38	-0.54	0.22	-	-	-	-		
TK1809	4-alpha-Glucanotransferase, GH57 family_COG	-0.54	-0.42	-0.48	0.09	2.79	0.13	1.46	1.88		
TK1810	Cytidylyltransferase_COG0170	-	-0.06	-	-	-	1.36	-	-		
TK1811	Hydrolase, HAD superfamily_COG1011	-0.55	-0.25	-0.40	0.21	-	-0.31	-	-		
TK1812	Hypothetical membrane protein, conserved, DU	-1.21	-1.02	-1.11	0.14	0.79	3.74	2.27	2.08		
TK1813	NapA-type sodium/hydrogen antiporter_COG0	-0.48	-0.36	-0.42	0.08	0.14	-0.36	-0.11	0.35		
TK1814	Tyrosine decarboxylase_COG0076	-0.19	-0.07	-0.13	0.08	1.06	-0.66	0.20	1.22		

TK1815	Transcription regulator, CopG/RepA family	-0.51	-0.53	-0.52	0.02	2.67	1.75	2.21	0.65		
TK1816	Hypothetical protein, conserved, flame shift	-0.61	0.16	-0.22	0.55	-	-	-	-		
TK1817	Cobalt/zinc/cadmium cation efflux pump prote	0.66	0.41	0.54	0.18	-	1.86	-	-		
TK1818	Hypothetical protein, conserved	5.58	5.21	5.39	0.26	1.83	1.09	1.46	0.52	5' (-26)	
TK1819	Capsular polysaccharide biosynthesis protein_C	0.00	-0.21	-0.10	0.15	-	-	-	-	5' (-162)	
TK1820	Membrane-associated metalloprotease, M50 fa	-0.33	-0.79	-0.56	0.32	-1.15	-0.67	-0.91	0.34		
TK1821	ATPase, PP-loop superfamily_COG0037	-0.04	-0.20	-0.12	0.11	-	-	-	-	coding	
TK1822	Predicted ATPase, AAA superfamily_COG1373	0.34	-0.12	0.11	0.33	-0.02	-0.25	-0.14	0.16		
TK1823	Hypothetical protein, conserved	0.56	-0.01	0.28	0.40	-	4.36	-	-		
TK1824	Hypothetical protein, conserved	-0.51	-0.57	-0.54	0.04	-	-0.51	-	-		
TK1825	Hypothetical membrane protein, conserved	-0.39	-0.23	-0.31	0.11	-	-	-	-		
TK1826	Predicted transcription regulator, ArsR family_C	-0.03	-0.26	-0.15	0.16	-	-0.46	-	-		
TK1827	Membrane-bound beta-glycosidase, GH1 family	-0.05	-0.33	-0.19	0.20	-	-0.49	-	-		
TK1828	Galactose-1-phosphate uridylyltransferase_CO	-0.92	-0.14	-0.53	0.55	-	4.97	-	-		
TK1829	Permease, major facilitator superfamily_COG04	-0.78	-0.66	-0.72	0.08	-	1.65	-	-	operon	
TK1830	Probable alpha-amylase, GH57 family_COG154	-	0.42	-	-	-	1.21	-	-	operon	
TK1831	Galactokinase_COG0153	-0.77	-0.80	-0.78	0.02	2.66	-	-	-	5' (-124)	
TK1832	Hypothetical membrane protein, conserved	0.33	-0.24	0.05	0.41	-	-	-	-		coding
TK1833	Hypothetical protein, conserved, containing DU	-0.41	-0.30	-0.36	0.07	-	-0.11	-	-	coding	coding
TK1834	Hypothetical protein	-0.43	-0.20	-0.31	0.17	-1.16	-1.41	-1.29	0.18		
TK1835	Pyrrolidone-carboxylate peptidase_COG2039	-0.64	-0.42	-0.53	0.16	-	-0.30	-	-		
TK1836	Geranylgeranyl hydrogenase_COG0644	-0.43	-0.16	-0.30	0.19	-0.62	-0.66	-0.64	0.03		
TK1837	Hypothetical protein, conserved, DUF1530 fam	-0.15	-0.10	-0.13	0.04	0.43	1.81	1.12	0.98		
TK1838	Hypothetical membrane protein	0.03	-0.47	-0.22	0.36	-	-0.14	-	-		
TK1839	Hypothetical protein, conserved	-0.62	-0.59	-0.60	0.03	-	1.13	-	-		coding
TK1840	Cobalt-activating carboxypeptidase, M32 family	-0.60	-0.73	-0.67	0.09	-0.53	-0.77	-0.65	0.17	coding	coding
TK1841	Predicted site-specific integrase-resolvase_CO	-0.43	-0.31	-0.37	0.08	-	-	-	-		
TK1842	Probable transposase_COG0675	-0.64	-0.33	-0.48	0.22	2.67	-0.41	1.13	2.17		
TK1843	Carbohydrate/pyrimidine kinase, PfkB family_C	-0.17	-0.10	-0.14	0.06	-	-0.82	-	-		
TK1844	Hypothetical membrane protein, conserved	-0.36	-0.35	-0.36	0.00	-	-	-	-		
TK1845	Hypothetical membrane protein, conserved, co	-0.85	-0.34	-0.60	0.36	7.58	-	-	-		
TK1846	MoxR-related ATPase, AAA superfamily_COG0	0.42	-0.01	0.21	0.31	-	-	-	-	coding	
TK1847	Hypothetical membrane protein, conserved	-0.50	-0.19	-0.35	0.21	1.43	0.24	0.84	0.84		
TK1848	Hypothetical membrane protein, conserved_CO	-	-0.10	-	-	-	-	-	-		
TK1849	Hypothetical protein, conserved_COG4072	0.21	0.25	0.23	0.03	-	-0.38	-	-	coding	
TK1850	FKBP-type peptidyl-prolyl cis-trans isomerase	0.96	0.62	0.79	0.24	-0.48	-1.43	-0.95	0.67		
TK1851	Hypothetical membrane protein, conserved_CO	1.00	0.83	0.91	0.12	0.07	0.03	0.05	0.03		
TK1852	Hypothetical membrane protein, conserved_CO	-0.63	-0.55	-0.59	0.06	0.35	0.31	0.33	0.03		
TK1853	Type II/IV secretion system ATPase; intein_CO	-0.78	-0.76	-0.77	0.02	-0.58	-0.77	-0.68	0.14		
TK1854	Hypothetical protein, conserved	-0.34	-0.36	-0.35	0.01	2.19	1.10	1.65	0.77		
TK1855	Hypothetical protein, conserved, DUF515 family	-0.69	-0.55	-0.62	0.10	-0.94	-0.48	-0.71	0.33		
TK1856	Hypothetical protein, conserved	-0.47	-0.44	-0.46	0.02	-0.55	0.80	0.13	0.95		
TK1857	GTPase, MMR1/HSR1 family_COG1161	-0.24	-0.06	-0.15	0.13	0.01	0.32	0.16	0.21		
TK1858	Predicted permease, containing FtsX domains	-0.02	-0.27	-0.14	0.18	-	-	-	-		coding
TK1859	Probable lipoprotein releasing system, ATP-bin	0.96	0.70	0.83	0.19	-	-0.53	-	-		
TK1860	ABC-type dipeptide/oligopeptide transport sys	0.81	1.06	0.93	0.17	-	0.00	-	-		
TK1861	ABC-type dipeptide/oligopeptide transport sys	0.07	0.12	0.09	0.03	-	-	-	-		
TK1862	Hypothetical protein	2.40	-	-	-	-	-	-	-	coding	
TK1863	Predicted N6-adenine-specific DNA methylase	-0.12	-0.20	-0.16	0.05	-	-0.36	-	-		
TK1864	ABC-type phosphate transport system, peripla	0.16	0.07	0.12	0.06	4.76	1.11	2.93	2.58		
TK1865	Predicted AP endonuclease_COG1082	-0.25	-0.16	-0.20	0.06	0.62	-	-	-		
TK1866	ABC-type phosphate transport system, perme	-0.80	-0.48	-0.64	0.23	-0.15	-	-	-		
TK1867	ABC-type phosphate transport system, perme	0.00	-0.26	-0.13	0.19	-	-	-	-		
TK1868	ABC-type phosphate transport system, ATPas	0.01	-0.46	-0.23	0.33	-	0.10	-	-		
TK1869	Probable phosphate transport system regulator	0.26	0.10	0.18	0.11	-	-	-	-		coding
TK1870	Phosphate transport system regulator_COG070	-0.52	-0.58	-0.55	0.04	-0.29	-	-	-	coding	
TK1871	Hypothetical protein, conserved	4.14	3.92	4.03	0.15	2.21	-	-	-		
TK1872	2-Hydroxyhepta-2,4-diene-1,7-dioate isomera	0.42	0.65	0.54	0.16	2.32	2.95	2.64	0.45		
TK1873	Hypothetical protein, conserved	1.57	1.54	1.56	0.02	-0.32	0.20	-0.06	0.37	coding	
TK1874	Tryptophanyl-tRNA synthetase_COG0180	0.51	0.28	0.40	0.16	-	-0.69	-	-	coding	
TK1875	Hypothetical protein, conserved, DUF104 family	-0.63	-0.36	-0.50	0.19	-	3.84	-	-		
TK1876	Permease, drug/metabolite transporter (DMT)	-0.33	-	-	-	-	1.28	-	-		
TK1877	Archaeal ATPase, fused to C-terminal DUF234	-0.12	-0.22	-0.17	0.07	-	1.96	-	-		
TK1878	Alkylphosphonate utilization protein PhnP hom	0.32	0.28	0.30	0.03	-	1.44	-	-		
TK1879	Hypothetical protein	3.37	3.31	3.34	0.05	1.26	-0.04	0.61	0.92		
TK1880	Archaeal succinyl-CoA synthetase (NDP formi	1.08	0.76	0.92	0.22	-1.11	-0.71	-0.91	0.28		
TK1881	Transcription regulator, ArsR family_COG0640	0.74	0.47	0.60	0.19	-0.73	-0.50	-0.61	0.16	coding	
TK1882	Hypothetical protein, conserved, DUF211 family	-0.16	0.14	-0.01	0.21	-0.62	-0.12	-0.37	0.36		
TK1883	Transcription regulator, ArsR family_COG0640	0.15	0.10	0.13	0.04	-0.90	-1.49	-1.20	0.42		
TK1884	alpha-Amylase precursor, GH13 family_COG03	-0.34	-0.48	-0.41	0.10	-	-0.04	-	-		
TK1885	Hypothetical protein	0.16	-0.04	0.06	0.14	-	-1.01	-	-		
TK1886	YjeF-ralted probable carbohydrate kinase_COG	0.53	0.39	0.46	0.10	0.38	-0.48	-0.05	0.61	coding	
TK1887	Hypothetical membrane protein	1.03	1.15	1.09	0.08	-	0.60	-	-	5' (+47)	coding
TK1888	Hypothetical membrane protein, conserved	1.67	1.68	1.67	0.01	-	0.69	-	-	coding	
TK1889	Hypothetical membrane protein	0.55	0.39	0.47	0.11	0.46	0.01	0.24	0.31		
TK1890	Histone macroH2A-related protein (C-terminus	0.08	-0.17	-0.04	0.17	-	-	-	-	coding	
TK1891	Probable guanine deaminase_COG0402	-0.24	-0.05	-0.15	0.13	0.35	-0.28	0.04	0.45	coding	
TK1892	Hypothetical protein, conserved, DUF553 family	1.17	1.14	1.15	0.03	0.39	0.40	0.39	0.01		
TK1893	Glycerate kinase-related protein, containing M	-	-0.13	-	-	-	-	-	-		
TK1894	Hypothetical membrane protein	-	0.06	-	-	-	-	-	-		
TK1895	Purine-nucleoside phosphorylase_COG0005	0.27	-0.16	0.06	0.31	2.05	-0.22	0.91	1.61	coding	
TK1896	Hypothetical protein, conserved, DUF75 family	0.89	0.49	0.69	0.29	-0.08	0.83	0.38	0.65		5' (-24)
TK1897	Hypothetical protein, conserved, DUF473 family	0.01	0.01	0.01	0.00	-0.26	0.95	0.34	0.86		operon
TK1898	Hypothetical protein, conserved, DUF91 family	-0.69	-0.29	-0.49	0.29	5.99	2.77	4.38	2.28		coding
TK1899	RadA/Rad51 recombinase; intein_COG0468	0.86	0.87	0.87	0.01	0.72	-0.49	0.11	0.85		
TK1900	Calcium-gated potassium channel protein_COG	0.26	0.12	0.19	0.10	2.44	2.36	2.40	0.05		
TK1901	Cell division control protein 6 homolog_COG14	0.77	0.14	0.45	0.44	-	0.32	-	-	coding	
TK1902	DNA polymerase II, small subunit_COG1311	-0.39	-0.27	-0.33	0.08	0.54	1.12	0.83	0.41	coding	
TK1903	DNA polymerase II, large subunit; intein_COG19	-1.02	-0.28	-0.65	0.53	1.36	-	-	-	coding	
TK1904	Hypothetical protein, conserved	0.08	0.17	0.12	0.07	-	-0.30	-	-		
TK1905	Hypothetical protein, conserved	-0.67	-	-	-	1.80	2.43	2.11	0.45	coding	

TK1906	Hypothetical protein	0.08	0.13	0.11	0.04	1.07	0.01	0.54	0.75	5' (-166)	
TK1907	Hypothetical protein, conserved, DUF207 family	-0.20	-0.08	-0.14	0.09	-	-	-	-		
TK1908	Lipoate-protein ligase A, N-terminal section_C	0.26	-0.14	0.06	0.28	-	-0.19	-	-		
TK1909	Dolichol-phosphate mannosyltransferase, fused	-0.30	-0.23	-0.27	0.04	-0.05	0.57	0.26	0.43		
TK1910	ATPase, RecA superfamily_COG0467	-0.90	-0.90	-0.90	0.01	-0.54	-0.68	-0.61	0.09		
TK1911	Hypothetical protein, conserved	-0.81	-0.81	-0.81	0.00	-0.38	-0.58	-0.48	0.14		
TK1912	Aminopeptidase, family M28, containing PA dor	-0.70	-0.70	-0.70	0.00	0.73	0.08	0.41	0.46	coding	
TK1913	Transcription regulator, ArsR family_COG5625	-0.54	-0.63	-0.58	0.07	-	-0.12	-	-	coding	
TK1914	Exonuclease SbcD homolog_COG1407	-0.14	0.00	-0.07	0.10	-	1.57	-	-		
TK1915	LSU ribosomal protein L41E	-0.54	-0.32	-0.43	0.16	-	1.51	-	-		
TK1916	Carbon-nitrogen hydrolase_COG0388	-0.66	-0.21	-0.43	0.31	0.15	3.50	1.82	2.37		
TK1917	Predicted SAM-dependent methyltransferase_(	1.40	0.99	1.20	0.29	1.72	0.03	0.87	1.20		
TK1918	Hypothetical membrane protein	-0.82	-0.54	-0.68	0.20	-	0.44	-	-		
TK1919	Hypothetical membrane protein	-0.45	-0.39	-0.42	0.04	2.13	-	-	-		
TK1920	Hypothetical protein, conserved	-0.33	-0.16	-0.25	0.12	-	-	-	-		
TK1921	Hypothetical membrane protein, conserved, fla	0.21	0.01	0.11	0.15	-0.54	0.04	-0.25	0.41		
TK1922	Hypothetical membrane protein, conserved, fla	-0.04	-0.34	-0.19	0.21	-	2.08	-	-		
TK1923	Hypothetical membrane protein, conserved_CO	-	0.08	-	-	1.94	-	-	-	coding	coding
TK1924	Transcription regulator, PadR-like family_COG1	0.35	-0.26	0.04	0.43	-	0.43	-	-		
TK1925	Hypothetical membrane protein, conserved	-0.58	-0.48	-0.53	0.07	1.41	1.12	1.26	0.20		
TK1926	Hypothetical protein, conserved, DUF74 family	0.10	0.07	0.09	0.02	-	1.06	-	-	coding	
TK1927	Hypothetical membrane protein, conserved_CO	1.69	1.67	1.68	0.01	-	-1.51	-	-	coding	
TK1928	Diphthine synthase, DPH2 subunit_COG1736	-1.07	-	-	-	-	-	-	-		
TK1929	Hypothetical protein, conserved	-0.66	-0.65	-0.65	0.01	0.02	0.87	0.45	0.60		
TK1930	Hypothetical protein	0.71	0.01	0.36	0.49	-	2.77	-	-		
TK1931	Hypothetical protein, conserved	-0.68	-0.47	-0.57	0.14	0.33	0.76	0.55	0.30		
TK1932	ATPase, RecA superfamily_COG0467	-	-0.13	-	-	-	-	-	-	coding	
TK1933	Predicted DNA methylase_COG2263	0.14	0.05	0.09	0.06	2.34	-0.13	1.10	1.75		
TK1934	Hypothetical protein, conserved	1.38	1.12	1.25	0.19	0.65	1.23	0.94	0.41		
TK1935	tRNA/rRNA cytosine-C5-methylase, NOL1/NO	0.16	-0.25	-0.05	0.30	-	-0.97	-	-	coding	
TK1936	ABC-type multidrug transport system, ATPase	0.12	0.32	0.22	0.14	-0.61	-1.46	-1.04	0.60		
TK1937	Hypothetical membrane protein, conserved	0.34	0.53	0.43	0.14	-0.34	0.92	0.29	0.89		
TK1938	ABC-type transport system, probable permeas	0.03	0.47	0.25	0.31	-0.05	-0.18	-0.12	0.10		
TK1939	Hypothetical protein, conserved	0.77	1.15	0.96	0.27	-	0.33	-	-	5' (+47)	5' (-46)
TK1940	Small-conductance mechanosensitive channel	-0.87	-0.59	-0.73	0.20	-	-0.28	-	-		
TK1941	Hypothetical protein, conserved, DUF432 family	-0.44	-0.46	-0.45	0.01	-	-	-	-		
TK1942	Hypothetical protein, conserved	-0.27	-0.37	-0.32	0.07	-	3.99	-	-		
TK1943	Hypothetical protein, conserved, containing DU	0.65	0.19	0.42	0.33	-0.78	-	-	-		
TK1944	Predicted metal-dependent phosphohydrolase,	0.16	0.12	0.14	0.03	1.15	0.94	1.04	0.14		
TK1945	Predicted nucleic acid-binding protein, contain	-0.82	-0.97	-0.90	0.11	0.04	-0.12	-0.04	0.11		
TK1946	Translation initiation factor eIF-2, gamma subu	-0.69	-0.43	-0.56	0.18	-0.73	-1.37	-1.05	0.46		
TK1947	Hypothetical membrane protein	1.12	1.25	1.19	0.09	-	1.78	-	-		
TK1948	Hypothetical membrane protein	2.90	2.87	2.89	0.02	2.43	0.39	1.41	1.44		
TK1949	Hypothetical protein	4.14	4.36	4.25	0.16	1.47	1.40	1.44	0.05	coding	
TK1950	Hypothetical protein	5.04	5.11	5.07	0.05	1.63	2.84	2.24	0.85	5' (-117)	
TK1951	SSU ribosomal protein S6E_COG2125	-0.13	0.21	0.04	0.24	-1.42	-0.82	-1.12	0.42		
TK1952	Preprotein translocase, SEC61 beta subunit	-0.79	-0.67	-0.73	0.08	-0.10	-	-	-		
TK1953	Hypothetical protein, conserved	-0.08	-0.30	-0.19	0.16	-0.34	-0.43	-0.39	0.06	coding	
TK1954	Probable GTP-binding protein_COG0218	-0.25	-0.09	-0.17	0.11	-	-	-	-		
TK1955	Predicted transcription regulator, Lrp/AsnC fa	0.55	0.30	0.42	0.18	-	-0.04	-	-		
TK1956	Hypothetical protein, conserved, containing AT	0.25	0.05	0.15	0.14	-2.36	0.26	-1.05	1.85		
TK1957	4-Hydroxybenzoate octaprenyltransferase_CO	0.39	0.27	0.33	0.08	1.63	1.93	1.78	0.21		
TK1958	Hypothetical protein, conserved	0.34	0.23	0.29	0.08	-0.98	-0.33	-0.65	0.45		
TK1959	Replication factor A complex, RPA32 subunit_C	2.67	2.38	2.53	0.21	0.24	0.80	0.52	0.40		
TK1960	Replication factor A complex, RPA14 subunit	0.49	2.04	1.27	1.09	0.12	0.47	0.30	0.25		
TK1961	Replication factor A complex, RPA41 subunit_C	2.08	2.23	2.16	0.10	-0.85	-1.93	-1.39	0.77		
TK1962	Predicted transcription regulator, YpuH-like fa	0.91	0.67	0.79	0.17	0.18	0.57	0.38	0.28	coding	
TK1963	NADP-dependent malic enzyme_COG0281	-0.52	-0.55	-0.53	0.02	0.49	-	-	-		
TK1964	Probable fumarate hydratase, beta subunit_CO	-0.53	-0.67	-0.60	0.10	0.27	-	-	-		
TK1965	Probable fumarate hydratase, alpha subunit_CO	-0.89	-0.79	-0.84	0.07	0.43	-0.94	-0.25	0.97		
TK1966	D-3-Phosphoglycerate dehydrogenase_COG01	0.46	0.13	0.30	0.23	-0.53	0.29	-0.12	0.58		
TK1967	Distant homolog of phosphate transport syster	-0.92	-0.65	-0.79	0.20	-0.41	-0.65	-0.53	0.17		
TK1968	2-Dehydropantoate 2-reductase_COG1893	-0.39	-0.42	-0.41	0.02	-	-0.72	-	-		
TK1969	Hypothetical membrane protein	0.11	-0.13	-0.01	0.17	0.39	1.11	0.75	0.51		
TK1970	Probable tRNA/rRNA methyltransferase, SpoU	-0.58	-0.46	-0.52	0.08	1.84	1.40	1.62	0.31		
TK1971	Methylated-DNA-protein-cysteine S-methyltra	-0.85	-0.89	-0.87	0.02	0.16	0.09	0.12	0.05		
TK1972	Hypothetical membrane protein, conserved, co	-0.23	-0.07	-0.15	0.11	-	-0.70	-	-	coding	
TK1973	Transcription factor, nascent polypeptide-asso	-0.70	-0.61	-0.65	0.06	1.14	-0.11	0.51	0.88		
TK1974	Carboxymuconolactone decarboxylase-related	-0.94	-0.78	-0.86	0.11	-	-1.40	-	-		
TK1975	Hypothetical protein, conserved	-0.10	-0.58	-0.34	0.34	-	1.56	-	-		
TK1976	HflX-related GTP-binding protein_COG2262	-0.29	-0.35	-0.32	0.04	1.73	-0.90	0.42	1.86	coding	
TK1977	Sodium/phosphate symporter_COG0306	-0.31	-0.08	-0.19	0.17	-0.30	-0.10	-0.20	0.15	coding	
TK1978	Pyruvate/2-oxoisovalerate: ferredoxin oxidored	-0.94	-0.85	-0.90	0.07	-0.71	-0.86	-0.78	0.11		
TK1979	2-Oxoisovalerate:ferredoxin oxidoreductase, de	0.07	-0.21	-0.07	0.20	-1.63	-1.04	-1.34	0.41		
TK1980	2-Oxoisovalerate:ferredoxin oxidoreductase, al	-0.47	-0.45	-0.46	0.01	-0.57	-0.20	-0.38	0.27	coding	
TK1981	2-Oxoisovalerate:ferredoxin oxidoreductase, be	-1.23	-0.91	-1.07	0.23	-0.63	-1.02	-0.82	0.27	5' (+18)	
TK1982	Pyruvate:ferredoxin oxidoreductase, delta subu	0.06	-0.15	-0.05	0.14	-1.31	-0.86	-1.08	0.32		
TK1983	Pyruvate:ferredoxin oxidoreductase, alpha subu	-0.19	-0.34	-0.26	0.11	-1.66	-1.41	-1.54	0.18		
TK1984	Pyruvate:ferredoxin oxidoreductase, beta subu	0.04	-0.18	-0.07	0.16	-1.61	-0.99	-1.30	0.44	coding	
TK1985	Hypothetical membrane protein	0.03	-0.36	-0.17	0.28	0.15	0.48	0.32	0.23		
TK1986	Hypothetical protein	-	-0.60	-	-	-0.68	0.03	-0.33	0.50		coding
TK1987	Hypothetical protein	-0.48	-0.39	-0.44	0.07	-0.25	1.90	0.83	1.52		
TK1988	Hypothetical protein, containing leucine zipper	-	-0.38	-	-	-	-	-	-		
TK1989	Hypothetical protein, conserved (C-terminus)	-0.01	-0.33	-0.17	0.22	-0.81	1.02	0.11	1.30	coding	
TK1990	Cysteine desulfurase_COG0520	-0.98	-0.36	-0.67	0.44	-0.96	-0.93	-0.94	0.02		coding
TK1991	Hypothetical protein, conserved	0.03	-0.09	-0.03	0.08	-0.01	0.01	0.00	0.01		
TK1992	Permease, major facilitator superfamily_COG04	-1.19	-0.53	-0.86	0.46	-	0.93	-	-		
TK1993	Hydrogenase expression/formation protein Hyp	-1.09	-0.82	-0.95	0.20	-0.01	-0.43	-0.22	0.29		
TK1994	Nucleotidyltransferase	-0.19	-0.54	-0.37	0.24	-0.49	-0.31	-0.40	0.13		
TK1995	Predicted nucleic acid-binding protein, contain	-0.07	-0.38	-0.23	0.22	0.10	-0.77	-0.34	0.61		
TK1996	Hypothetical protein	-0.28	-0.52	-0.40	0.17	-0.62	-0.51	-0.56	0.08		

TK1997	Hydrogenase maturation protein HypF_COG006	-1.12	-1.00	-1.06	0.09	-0.41	-0.99	-0.70	0.41	coding	
TK1998	Hypothetical protein, conserved	0.04	0.11	0.08	0.05	-2.04	-2.15	-2.09	0.08		coding
TK1999	Ferritin_COG1528	-0.95	-0.46	-0.71	0.35	-0.64	-0.12	-0.38	0.37		
TK2000	Hydrogenase expression/formation protein hyp	-0.31	-0.42	-0.36	0.08	-0.61	-0.86	-0.74	0.17	coding	
TK2001	Hydrogenase expression/formation protein Hyp	-1.42	-0.90	-1.16	0.37	-	-	-	-		
TK2002	Molybdopterin-guanine dinucleotide biosynthes	-1.45	-	-	-	-1.89	-1.60	-1.74	0.21		
TK2003	Hypothetical protein	-0.03	-0.06	-0.04	0.03	-	-	-	-		
TK2004	Hydrogenase maturation protease HycI_COG06	-	-0.38	-	-	-	-0.44	-	-		
TK2005	Predicted nucleic acid-binding protein, containi	-0.10	-0.33	-0.22	0.16	-	-1.13	-	-		
TK2006	Hypothetical protein, conserved	-0.38	-0.29	-0.34	0.06	-0.76	-0.77	-0.76	0.01		
TK2007	ATPase involved in chromosome partitioning, P	-0.40	-0.43	-0.41	0.02	-0.90	-1.43	-1.17	0.37	coding	
TK2008	Hydrogenase nickel-incorporation protein HypA	-0.33	-0.52	-0.42	0.14	-0.64	-0.73	-0.69	0.07		
TK2009	Cobalt/zinc/cadmium cation efflux pump prote	-0.02	-0.15	-0.08	0.09	-	0.24	-	-		
TK2010	Iron-molybdenum cofactor-binding protein, flar	-	-0.15	-	-	-	-	-	-		
TK2011	Iron-molybdenum cofactor-binding protein, flar	-0.33	-0.18	-0.26	0.10	-	-	-	-		
TK2012	Ferredoxin 3_COG1146	-0.31	-0.34	-0.32	0.02	-	-0.65	-	-		
TK2013	Hypothetical protein	-0.60	-0.38	-0.49	0.15	-	-0.47	-	-	coding	coding
TK2014	Hypothetical membrane protein, conserved, DU	-1.06	-0.53	-0.80	0.38	-	2.05	-	-		
TK2015	C4-Dicarboxylate transporter_COG1275	-0.62	-0.45	-0.54	0.12	2.13	3.42	2.78	0.91		
TK2016	Iron-molybdenum cofactor-binding protein_CO	-0.52	-0.47	-0.50	0.04	0.46	3.87	2.17	2.41		
TK2017	Predicted stress-inducible protein, OsmC/Ohr	-0.40	-0.35	-0.38	0.03	0.20	0.04	0.12	0.11		
TK2018	ABC-type iron(III)-siderophore transport syste	-0.66	-0.32	-0.49	0.24	0.26	0.20	0.23	0.05		
TK2019	ABC-type iron(III)-siderophore transport syste	-0.56	-0.39	-0.47	0.12	0.54	1.15	0.85	0.43		coding
TK2020	ABC-type iron(III)-siderophore transport syste	0.13	-0.18	-0.02	0.22	-	-0.35	-	-	coding	
TK2021	ATPase involved in chromosome partitioning, P	-0.38	-0.39	-0.39	0.01	-0.68	-1.05	-0.86	0.27		
TK2022	Hypothetical membrane protein, conserved	-	-0.20	-	-	-	-	-	-		5' (-137)
TK2023	Hypothetical protein, conserved_COG4044	0.62	0.09	0.36	0.37	-	-0.24	-	-		
TK2024	Transcription initiation factor IIE, alpha subunit	-0.76	-0.48	-0.62	0.20	-	-1.03	-	-		
TK2025	Hypothetical protein, conserved	0.37	0.03	0.20	0.25	-0.52	-0.87	-0.70	0.25		
TK2026	ABC-type multidrug transport system, ATPase	-0.86	-0.42	-0.64	0.31	-	1.94	-	-		
TK2027	ABC-type multidrug transport system, permea	-0.62	-0.52	-0.57	0.07	-	-0.72	-	-		
TK2028	ABC-type multidrug transport system, permea	0.46	0.26	0.36	0.14	-	5.62	-	-		
TK2029	Carbohydrate/pyrimidine kinase, PfkB family_C	-0.73	-0.39	-0.56	0.24	0.01	0.01	0.01	0.00		
TK2030	Hypothetical protein, conserved	-1.28	-0.78	-1.03	0.36	0.27	0.27	0.27	0.00		
TK2031	Acylphosphatase_COG1254	-0.55	-0.58	-0.57	0.02	0.42	0.82	0.62	0.28		
TK2032	Periplasmic divalent cation tolerance protein_C	-0.31	-0.31	-0.31	0.00	-0.53	-0.12	-0.32	0.29		
TK2033	Hypothetical protein, conserved, DUF99 family	-0.36	-0.45	-0.40	0.07	0.38	-0.23	0.08	0.43		
TK2034	Universal stress protein_COG0589	-0.19	-0.33	-0.26	0.10	-	-	-	-		
TK2035	Glycine cleavage system protein T (aminometh	-0.52	-0.48	-0.50	0.03	-1.55	-1.56	-1.56	0.01		
TK2036	Permease, drug/metabolite transporter (DMT)	-0.10	-0.29	-0.19	0.14	0.32	0.25	0.29	0.05		
TK2037	Signal peptidase I_COG0681	-0.10	-0.25	-0.17	0.11	0.03	-0.40	-0.19	0.30	coding	
TK2038	Hypothetical protein, conserved, DUF531 famil	0.14	-0.08	0.03	0.16	-	0.72	-	-		
TK2039	Hypothetical protein, conserved, containing TP	0.32	0.00	0.16	0.23	0.55	1.02	0.79	0.33		
TK2040	Microsomal dipeptidase homolog_COG2355	-0.68	-0.46	-0.57	0.16	-	-	-	-	coding	
TK2041	Hypothetical protein, conserved	-0.20	0.10	-0.05	0.21	0.35	0.71	0.53	0.26	coding	
TK2042	ATPase, RecA superfamily_COG0467	0.00	0.10	0.05	0.08	0.12	-0.08	0.02	0.14		
TK2043	Hypothetical protein, conserved, DUF257 famil	-0.06	-0.29	-0.17	0.17	0.57	3.86	2.21	2.32		
TK2044	Hypothetical protein, conserved, DUF257 famil	-0.90	-0.25	-0.57	0.46	-	-0.73	-	-		
TK2045	SAM-dependent methyltransferase, UPF0020 f	0.04	-0.06	-0.01	0.07	-	1.01	-	-		
TK2046	Hypothetical membrane protein	-0.80	-0.65	-0.72	0.11	-	-0.10	-	-		
TK2047	Hypothetical membrane protein, conserved, DU	-0.30	-0.48	-0.39	0.13	-	1.07	-	-		
TK2048	Hypothetical protein	-0.67	-0.73	-0.70	0.04	-	-0.77	-	-	coding	coding
TK2049	Acylamino acid-releasing enzyme (acylaminoac	0.16	0.22	0.19	0.04	0.13	0.05	0.09	0.05		
TK2050	Hypothetical membrane protein, conserved	0.55	0.45	0.50	0.07	-	0.27	-	-	coding	
TK2051	Hypothetical protein, conserved_COG2112	-	0.50	-	-	-	0.78	-	-		
TK2052	Predicted transcription regulator, Lrp/AsnC fa	1.39	0.80	1.10	0.42	-	-0.95	-	-		
TK2053	ABC-type multidrug transport system, ATPase	2.86	3.07	2.96	0.15	0.15	-0.46	-0.15	0.43		operon
TK2054	ABC-type transport system, probable permeas	1.54	1.57	1.55	0.02	-	2.03	-	-		operon
TK2055	ABC-type transport system, probable permeas	0.33	0.22	0.27	0.08	-2.40	-	-	-		operon
TK2056	Hypothetical membrane protein	-0.23	0.33	0.05	0.40	-	-0.79	-	-		5' (-166)
TK2057	ABC-type dipeptide/oligopeptide transport sys	0.06	0.48	0.27	0.30	3.27	2.59	2.93	0.48	coding	
TK2058	ABC-type dipeptide/oligopeptide transport sys	2.86	2.51	2.69	0.25	0.31	-0.04	0.14	0.25		
TK2059	Hypothetical protein	-	1.88	-	-	-2.17	-1.20	-1.68	0.68	5' (-44)	
TK2060	Distant homolog of phosphate transport syster	-0.02	-0.26	-0.14	0.17	-	-1.43	-	-		
TK2061	Sodium/phosphate symporter_COG0306	-	-0.42	-	-	-	-0.56	-	-	coding	
TK2062	Metallophosphoesterase, calcineurin superfami	-0.19	-0.15	-0.17	0.03	0.11	1.06	0.59	0.67		
TK2063	Hypothetical protein, conserved, cupin superfa	-0.88	-0.54	-0.71	0.24	-0.63	-0.30	-0.47	0.23		
TK2064	Probable 2-methylthioadenine synthetase_COG	0.05	0.29	0.17	0.17	-1.40	-1.43	-1.41	0.02		
TK2065	Predicted RNA-binding protein, containing TRA	-0.10	-0.32	-0.21	0.15	-	-0.15	-	-		
TK2066	Hydrogenase-specific maturation endopeptidas	-0.42	-0.51	-0.46	0.07	0.07	-0.26	-0.10	0.23		
TK2067	Predicted nucleic acid-binding protein, containi	0.38	0.11	0.25	0.19	0.73	0.59	0.66	0.10		
TK2068	Hypothetical protein, conserved	-0.19	-0.39	-0.29	0.14	-	0.22	-	-		
TK2069	Cytosolic NiFe-hydrogenase, alpha subunit_CO	0.02	-0.05	-0.01	0.05	-1.22	-1.49	-1.36	0.20		coding
TK2070	Cytosolic NiFe-hydrogenase, delta subunit_CO	0.05	-0.22	-0.09	0.19	-1.05	-0.69	-0.87	0.26	coding	
TK2071	Cytosolic NiFe-hydrogenase, gamma subunit_C	-0.39	-0.37	-0.38	0.01	-0.69	-0.76	-0.73	0.06	coding	
TK2072	Cytosolic NiFe-hydrogenase, beta subunit_COG	-0.66	-0.72	-0.69	0.04	-2.11	-0.80	-1.46	0.93		coding
TK2073	4Fe-4S cluster-binding protein	-0.78	-0.91	-0.85	0.09	-0.18	-0.70	-0.44	0.37		
TK2074	Glutamate synthase beta chain-related oxidore	-1.12	-0.77	-0.95	0.25	-1.30	-0.96	-1.13	0.24		
TK2075	4Fe-4S cluster-binding protein_COG0437	0.00	-0.23	-0.11	0.16	-0.51	-0.41	-0.46	0.07		
TK2076	Formate:ferredoxin oxidoreductase, alpha subu	-0.53	-0.57	-0.55	0.03	-1.10	-1.01	-1.06	0.06	coding	
TK2077	Formate:ferredoxin oxidoreductase, 4Fe-4S clu	-0.74	-0.55	-0.65	0.13	-0.81	-1.32	-1.07	0.36		
TK2078	Formate:ferredoxin oxidoreductase, 4Fe-4S clu	-1.09	-0.90	-0.99	0.14	-0.70	-1.32	-1.01	0.44		
TK2079	Probable formate transporter_COG2116	-0.65	-0.49	-0.57	0.12	-1.06	-1.37	-1.21	0.22	coding	
TK2080	Membrane bound hydrogenase, MbhA subunit (	-0.55	-0.70	-0.62	0.11	-1.07	-0.88	-0.98	0.13		
TK2081	Membrane bound hydrogenase, MbhB subunit (	-0.67	-0.68	-0.67	0.01	-0.56	0.41	-0.08	0.69		
TK2082	Membrane bound hydrogenase, MbhC subunit (	-0.22	-0.44	-0.33	0.15	-0.67	-0.72	-0.70	0.03		
TK2083	Membrane bound hydrogenase, MbhD subunit (	0.02	-0.35	-0.17	0.26	-0.19	-0.53	-0.36	0.24		
TK2084	Membrane bound hydrogenase, MbhE subunit (	-0.85	-0.86	-0.85	0.01	-0.97	-0.86	-0.92	0.08		
TK2085	Membrane bound hydrogenase, MbhF subunit (	-0.74	-0.81	-0.77	0.04	-1.25	-0.96	-1.11	0.20		
TK2086	Membrane bound hydrogenase, MbhG subunit (	-0.32	-0.48	-0.40	0.11	-1.35	-1.08	-1.22	0.19		
TK2087	Membrane bound hydrogenase, MbhH subunit (	-0.75	-0.70	-0.72	0.03	-1.14	-0.71	-0.93	0.30		

TK2088	Membrane bound hydrogenase, MbhI subunit	-0.17	-0.57	-0.37	0.28	-0.94	-0.82	-0.88	0.08		
TK2089	Membrane bound hydrogenase, NiFe-hydrogena	-1.03	-0.88	-0.95	0.10	-0.83	-1.29	-1.06	0.33	coding	
TK2090	Membrane bound hydrogenase, NiFe-hydrogena	-0.37	-0.48	-0.42	0.08	-0.95	-0.92	-0.93	0.02		
TK2091	Membrane bound hydrogenase, NiFe-hydrogena	-0.62	-0.48	-0.55	0.10	-0.74	-1.11	-0.92	0.26	coding	coding
TK2092	Membrane bound hydrogenase, MbhM subunit_(	-0.08	-0.03	-0.06	0.03	-0.63	-0.89	-0.76	0.19		
TK2093	Membrane bound hydrogenase, 4Fe-4S cluster	0.03	0.03	0.03	0.00	-1.03	-0.97	-1.00	0.04		
TK2094	Rubrerythrin-related protein_COG1633	0.63	0.10	0.36	0.37	-1.21	-1.19	-1.20	0.01		
TK2095	Rubrerythrin-related protein	0.05	0.05	0.05	0.01	-	-0.98	-	-		
TK2096	Rubrerythrin-related protein_COG1633	0.28	0.19	0.24	0.07	-0.18	-0.30	-0.24	0.08		
TK2097	RNA-binding protein, containing THUMP domai	0.02	-0.11	-0.05	0.09	-	-0.10	-	-		
TK2098	Predicted ATPase, AAA superfamily	-0.33	-0.34	-0.33	0.00	-0.71	-1.13	-0.92	0.30		
TK2099	Predicted membrane-bound metal-dependent I	-0.89	-0.81	-0.85	0.06	0.30	-0.59	-0.14	0.63	coding	
TK2100	Thioredoxin reductase_COG0492	-0.19	-0.36	-0.28	0.12	-2.37	-1.27	-1.82	0.78	coding	
TK2101	Aminotransferase, class III_COG0160	-0.03	0.09	0.03	0.09	-1.37	-1.84	-1.61	0.33	coding	
TK2102	Hypothetical membrane protein, conserved, DU	0.51	0.36	0.44	0.11	-0.52	-0.16	-0.34	0.25		
TK2103	Hypothetical protein, conserved	-0.29	0.16	-0.06	0.32	-0.30	0.28	-0.01	0.41		
TK2104	Deoxyribose-phosphate aldolase_COG0274	0.31	0.30	0.31	0.00	-0.13	-0.50	-0.32	0.27		
TK2105	Hypothetical protein, conserved	-0.22	-0.22	-0.22	0.00	0.42	-0.43	-0.01	0.60		
TK2106	Enolase_COG0148	-0.20	-0.42	-0.31	0.16	-	-0.65	-	-	coding	
TK2107	Transcription regulator, PadR-like family	-0.40	0.01	-0.19	0.28	1.60	1.05	1.33	0.39		
TK2108	Hypothetical membrane protein, conserved	-0.50	-0.37	-0.44	0.09	-0.11	-1.29	-0.70	0.83		
TK2109	Biotin synthase-related protein, radical SAM su	0.28	0.11	0.20	0.12	0.41	1.87	1.14	1.04		
TK2110	Transcription regulator, Lrp/AsnC family_COG1	-0.04	0.03	-0.01	0.05	-	-0.43	-	-		
TK2111	Nucleoside triphosphate phosphohydrolase, Ha	-	-0.38	-	-	-1.26	-1.28	-1.27	0.01		
TK2112	Hypothetical protein, conserved, DUF355 family	-0.15	-0.02	-0.08	0.09	0.71	0.24	0.47	0.33		
TK2113	Hypothetical protein, conserved_COG1522	-0.13	0.06	-0.03	0.13	3.68	3.34	3.51	0.24		
TK2114	Hypothetical protein, conserved_COG0535	3.96	3.52	3.74	0.32	1.76	0.75	1.26	0.72		
TK2115	Molybdopterin converting factor, subunit 2_CO(	-0.03	-0.13	-0.08	0.07	-0.46	-0.45	-0.45	0.01	coding	
TK2116	Hypothetical protein	-0.13	-0.20	-0.16	0.05	0.84	-0.92	-0.04	1.25	coding	
TK2117	Molybdenum cofactor biosynthesis protein Moe	-0.21	-0.31	-0.26	0.07	-	-1.12	-	-		
TK2118	Molybdopterin converting factor, subunit 1_CO(	-0.40	-0.42	-0.41	0.01	-	1.66	-	-		
TK2119	Hypothetical membrane protein, conserved, DU	-0.40	-0.41	-0.41	0.01	0.02	-0.17	-0.08	0.13		
TK2120	Hypothetical protein, conserved, containing DU	-0.51	-0.44	-0.48	0.06	0.65	0.42	0.54	0.17		
TK2121	Hypothetical protein, conserved	0.72	0.20	0.46	0.37	1.01	0.22	0.62	0.56		
TK2122	tRNA/rRNA cytosine-C5-methylase, NOL1/NO(	0.11	0.14	0.13	0.03	-0.32	0.32	0.00	0.45		
TK2123	Hypothetical membrane protien, conserved, UP	-	0.11	-	-	-	-	-	-		
TK2124	ATP-NAD kinase_COG0061	0.12	-0.06	0.03	0.13	-0.43	-	-	-		
TK2125	Hypothetical membrane protein, conserved, co	-1.24	-0.82	-1.03	0.30	-0.39	0.27	-0.06	0.47		
TK2126	O-Sialoglycoprotein endopeptidase_COG0533	0.01	0.05	0.03	0.03	-0.51	-2.64	-1.57	1.51		
TK2127	Acyl-CoA synthetase (NDP forming), large sub	-0.44	-0.39	-0.41	0.04	-	-0.08	-	-		
TK2128	Phosphopantetheine adenylyltransferase_COG1	0.82	0.14	0.48	0.48	-0.17	-0.86	-0.52	0.49		
TK2129	Triosephosphate isomerase_COG0149	-0.16	-0.21	-0.18	0.03	-0.09	0.61	0.26	0.49		
TK2130	ATP:corrinoid adenosyltransferase_COG2109	-0.28	-0.36	-0.32	0.05	0.18	0.03	0.10	0.11		
TK2131	Hypothetical protein, conserved, UPF0147 fami	-0.55	-0.19	-0.37	0.26	-1.53	-0.89	-1.21	0.45		
TK2132	Fuculose-1-phosphate aldolase_COG0235	-0.48	-0.24	-0.36	0.17	-	0.70	-	-		
TK2133	Hypothetical protein, conserved	-0.65	-0.24	-0.44	0.29	-	-	-	-		coding
TK2134	Transcription regulator, Lrp/AsnC family_COG1	0.52	0.29	0.41	0.16	-0.94	-0.35	-0.64	0.41		coding
TK2135	23S rRNA (uracil-5-)-methyltransferase_COG2	0.04	0.01	0.02	0.02	-	-	-	-		
TK2136	Hypothetical protein, conserved	-0.74	-0.50	-0.62	0.17	0.24	-	-	-		
TK2137	ATPase involved in chromosome partitioning, P	0.04	-0.06	-0.01	0.07	-0.04	-0.67	-0.35	0.44		
TK2138	Orotate phosphoribosyltransferase_COG0461	0.78	0.60	0.69	0.13	-0.36	-0.10	-0.23	0.18		
TK2139	Hypothetical membrane protein, conserved	0.47	0.50	0.49	0.02	3.55	0.95	2.25	1.84		
TK2140	ATP-dependent DNA ligase_COG1793	0.20	0.07	0.13	0.09	-0.52	-0.96	-0.74	0.31		coding
TK2141	GHMP kinase_COG1829	-0.99	-1.27	-1.13	0.19	-0.70	-0.31	-0.50	0.28		
TK2142	NhaC-type sodium/hydrogen antiporter_COG1	-	-0.63	-	-	-	-1.79	-	-	coding	
TK2143	Uracil-DNA glycosylase_COG1573	0.45	0.25	0.35	0.15	0.17	0.40	0.28	0.17		
TK2144	Hypothetical protein, conserved	0.33	0.25	0.29	0.06	0.13	-0.15	-0.01	0.20		
TK2145	Hypothetical protein, conserved, radical SAM s	1.39	1.28	1.33	0.07	-0.72	-0.70	-0.71	0.01	coding	
TK2146	Hypothetical protein, conserved	1.15	0.95	1.05	0.14	-0.63	-0.87	-0.75	0.17		
TK2147	Methyl-accepting chemotaxis protein_COG084(	-1.03	-1.05	-1.04	0.01	0.52	-0.73	-0.10	0.89		
TK2148	Hypothetical protein, conserved_COG4697	-0.94	-0.52	-0.73	0.30	1.48	1.18	1.33	0.21	coding	
TK2149	Putative effector of murein hydrolase_COG138	-0.20	-0.47	-0.33	0.19	-	-0.51	-	-		
TK2150	Putative effector of murein hydrolase_COG134	-0.80	-0.99	-0.89	0.14	0.32	-0.37	-0.03	0.49		coding
TK2151	Archaeal transcription regulator_COG1356	-0.09	-0.18	-0.13	0.06	1.44	-0.10	0.67	1.09		
TK2152	Hypothetical protein, conserved, DUF431 family	0.04	-0.23	-0.10	0.19	-	0.71	-	-		
TK2153	Hypothetical protein, conserved	-0.68	-0.37	-0.52	0.22	0.67	1.26	0.97	0.42		
TK2154	Hypothetical protein, conserved, UPF0175 fami	-0.48	-0.33	-0.40	0.11	0.69	1.20	0.95	0.36		
TK2155	Predicted nucleic acid-binding protein, contain	-0.29	-0.13	-0.21	0.11	2.04	0.05	1.04	1.41		
TK2156	RNA-binding protein, containing PUA domain_C	-0.34	-0.23	-0.28	0.08	-	-1.26	-	-	coding	
TK2157	Hypothetical protein, conserved_COG1340	0.28	0.18	0.23	0.07	-1.21	-0.97	-1.09	0.17		
TK2158	Carbamate kinase-like carbamoyl phosphate sy	-0.28	-0.08	-0.18	0.14	0.26	0.95	0.61	0.49	coding	5' (-100)
TK2159	Predicted oxidoreductase_COG1233	-0.54	-0.21	-0.38	0.23	-	1.56	-	-		
TK2160	Hypothetical protein, conserved, radical SAM s	4.78	4.56	4.67	0.16	-	0.33	-	-	5' (-117)	
TK2161	ABC-type multidrug transport system, ATPase	4.65	4.36	4.50	0.20	0.27	0.71	0.49	0.31	operon	
TK2162	Hypothetical membrane protein, conserved	3.64	3.97	3.80	0.23	-	0.03	-	-	operon	
TK2163	Tungsten-containing glyceraldehyde-3-phosph	-0.68	-0.84	-0.76	0.11	-0.77	-	-	-	coding	
TK2164	Thermophile-specific fructose-1,6-bisphospha	-0.94	-0.69	-0.81	0.18	-1.72	-1.72	-1.72	0.00	coding	
TK2165	Hypothetical protein, conserved	0.29	0.16	0.23	0.09	0.12	1.38	0.75	0.89		
TK2166	ArgE/DapE-related deacylase_COG0624	-0.39	-0.37	-0.38	0.01	0.09	0.75	0.42	0.47	coding	
TK2167	3'-Phosphoadenosine 5'-phosphosulfate reduct	-0.04	-0.31	-0.18	0.19	-	1.30	-	-		
TK2168	Archaeal serine protease_COG1750	-0.11	0.03	-0.04	0.10	-0.16	-0.65	-0.41	0.35	coding	
TK2169	Zinc-dependent protease, TldD/PmbA family_C	0.17	0.05	0.11	0.09	-	0.05	-	-		
TK2170	Zinc-dependent protease, TldD/PmbA family_C	-0.45	-0.38	-0.42	0.05	-	0.04	-	-		coding
TK2171	Hypothetical protein, conserved, DUF257 family	-0.02	0.07	0.02	0.07	0.18	0.70	0.44	0.36	coding	
TK2172	Cyclodextrin glucanotransferase, GH13 family_(	-0.02	-0.12	-0.07	0.07	-0.46	-0.59	-0.52	0.09		
TK2173	Hypothetical protein, conserved	-0.11	-0.05	-0.08	0.05	-	-	-	-		
TK2174	Hypothetical protein	0.33	0.48	0.41	0.11	0.54	-	-	-		
TK2175	Hypothetical protein	2.21	2.19	2.20	0.01	2.37	1.67	2.02	0.50		
TK2176	Hypothetical protein	3.09	2.87	2.98	0.16	1.44	0.22	0.83	0.86		coding
TK2177	Hypothetical membrane protein	3.77	3.97	3.87	0.14	0.46	1.07	0.76	0.43	coding	
TK2178	Hypothetical protein, containing ATP/GTP-bin	3.97	4.28	4.12	0.22	0.60	0.45	0.52	0.11	5' (+23)	5' (+3)

TK2179	Hypothetical protein, conserved, BtpA family_C	-0.13	0.06	-0.03	0.13	-	-2.22	-	-		
TK2180	Hypothetical protein, conserved	0.30	0.00	0.15	0.21	2.31	-	-	-	coding	
TK2181	Predicted calcium-binding protein	-0.10	-0.05	-0.07	0.04	0.09	0.54	0.32	0.32	coding	
TK2182	Hypothetical protein	-	-0.09	-	-	-	2.91	-	-		
TK2183	Hypothetical protein, conserved	-0.01	0.02	0.01	0.02	4.97	4.87	4.92	0.07		
TK2184	Hypothetical protein, conserved	-	-0.22	-	-	-	-	-	-	coding	
TK2185	Phosphohexomutase_COG1109	-0.46	-0.31	-0.38	0.10	0.56	0.76	0.66	0.15		
TK2186	Predicted permease, containing DUF6 domain_C	-0.04	-0.35	-0.19	0.22	-	-	-	-	coding	
TK2187	Hypothetical membrane protein, conserved	-0.63	-0.57	-0.60	0.04	0.50	-0.88	-0.19	0.98		
TK2188	Hypothetical membrane protein, conserved	-	-0.23	-	-	-	1.65	-	-		
TK2189	Hypothetical membrane protein	0.08	-0.11	-0.02	0.13	1.33	1.69	1.51	0.25		
TK2190	Predicted transcription regulator, ArsR family_C	-0.20	-0.19	-0.19	0.01	0.28	-0.43	-0.08	0.50	coding	
TK2191	Hypothetical protein, conserved_COG5418	0.33	-0.03	0.15	0.26	-	1.71	-	-		
TK2192	Dephospho-CoA kinase_COG0237	0.53	0.43	0.48	0.07	-	-0.04	-	-		
TK2193	Hypothetical protein, conserved	0.37	-0.03	0.17	0.28	-0.87	-0.11	-0.49	0.53		
TK2194	Hypothetical membrane protein, conserved_CO	-1.53	-1.58	-1.56	0.04	-	-1.64	-	-	coding	
TK2195	Aspartate carbamoyltransferase, regulatory sul	-1.55	-1.52	-1.54	0.02	-1.81	-1.72	-1.77	0.06		
TK2196	Aspartate carbamoyltransferase, catalytic subu	-1.91	-1.90	-1.91	0.01	-1.53	-1.28	-1.41	0.18		
TK2197	Predicted transcription regulator, fused to C-t	1.67	1.62	1.65	0.03	0.17	-0.49	-0.16	0.47		
TK2198	Hypothetical protein, conserved, UPF0047 fami	1.37	1.44	1.41	0.05	0.09	0.85	0.47	0.54		
TK2199	Hypothetical protein	0.22	0.92	0.57	0.50	-1.08	-0.75	-0.91	0.23		coding
TK2200	Hypothetical protein, conserved_COG2403	0.58	0.21	0.40	0.26	-1.43	-1.21	-1.32	0.16	coding	
TK2201	Hypothetical membrane protein	1.56	1.37	1.46	0.14	-	-0.16	-	-		
TK2202	Predicted ATPase, AAA superfamily_COG1373	0.10	-0.17	-0.04	0.19	-	3.16	-	-		
TK2203	Hypothetical protein, conserved_COG3885	0.81	1.06	0.94	0.18	0.73	-0.65	0.04	0.98		
TK2204	Hypothetical protein, conserved	3.19	3.64	3.42	0.32	1.06	0.79	0.92	0.19	5' (-103)	
TK2205	Threonine synthase_COG0498	0.20	0.26	0.23	0.04	4.51	0.00	2.25	3.19	coding	
TK2206	Hypothetical protein, conserved	-0.61	-0.41	-0.51	0.14	-0.74	-	-	-		
TK2207	Proteasome, beta subunit 2_COG0638	-0.53	-0.48	-0.50	0.03	-0.38	-1.30	-0.84	0.65		
TK2208	ABC-type iron(III)-siderophore transport syste	-0.56	-0.28	-0.42	0.20	0.00	-0.77	-0.38	0.55		
TK2209	ABC-type iron(III)-siderophore transport syste	-0.58	-0.26	-0.42	0.23	-0.04	-0.32	-0.18	0.20	coding	
TK2210	5'-3' Nuclease, encoded next to Rad50 and Mr	0.52	0.43	0.47	0.06	-0.10	0.32	0.11	0.30	coding	
TK2211	DNA double-strand break repair ATPase Rad5	1.32	1.18	1.25	0.10	-0.63	-1.58	-1.11	0.67		
TK2212	DNA repair exonuclease Rad32/Mre11 homolog	0.14	-0.33	-0.09	0.33	-0.48	-0.92	-0.70	0.31		
TK2213	Bipolar DNA helicase_COG0433	0.55	0.68	0.61	0.10	-	-0.62	-	-	5' (+40)	
TK2214	Ribosomal protein-alanine acetyltransferase Ri	0.21	0.01	0.11	0.14	-	-0.68	-	-		
TK2215	Archaeal tRNA-intron endonuclease_COG1676	-0.37	-0.39	-0.38	0.02	0.11	-	-	-		
TK2216	Hypothetical membrane protein, conserved	0.55	-0.04	0.25	0.41	-	0.75	-	-		
TK2217	2-Amino-3-oxobutyrate coenzyme A ligase (gl	-0.40	-0.21	-0.31	0.13	-1.17	-1.37	-1.27	0.14		
TK2218	Replication factor C, small subunit; intein_COG	-0.18	-0.14	-0.16	0.03	0.99	0.13	0.56	0.61		coding
TK2219	Replication factor C, large subunit_COG0470	-0.50	-0.37	-0.44	0.09	-0.43	-1.09	-0.76	0.47		
TK2220	Archaeal ATPase_COG1373	-0.62	-0.20	-0.41	0.30	-	0.03	-	-		
TK2221	Hypothetical protein	-0.56	-0.47	-0.51	0.06	0.76	-0.77	0.00	1.09		
TK2222	Archaeal ATPase_COG1672	-0.10	-0.05	-0.07	0.03	1.68	-0.75	0.46	1.71		
TK2223	Met-10+ like protein_COG2520	-0.59	-0.19	-0.39	0.28	0.63	-	-	-		
TK2224	Hypothetical membrane protein, conserved, co	-0.80	-0.55	-0.67	0.17	3.49	-	-	-		
TK2225	Molybdenum cofactor biosynthesis protein A_C	-0.12	0.02	-0.05	0.10	-0.17	-0.33	-0.25	0.11		
TK2226	Hypothetical protein, conserved	-0.29	-0.29	-0.29	0.00	1.04	4.88	2.96	2.72		
TK2227	RNA-binding protein FAU-1_COG1530	0.12	-0.01	0.05	0.09	0.12	-0.51	-0.20	0.44		
TK2228	Predicted nucleic acid-binding protein, containi	-0.18	-0.23	-0.20	0.04	-0.65	1.28	0.31	1.36		
TK2229	Transcription regulator, SpoVT/AbrB family_C	-0.47	-0.21	-0.34	0.18	-	2.96	-	-		
TK2230	Hypothetical protein	-0.03	-0.05	-0.04	0.02	-	-	-	-		
TK2231	RadB recombinase_COG0468	-0.28	-0.41	-0.34	0.09	-	-1.11	-	-		coding
TK2232	Hydrolase, metallo-beta-lactamase superfamily	-0.75	-0.51	-0.63	0.16	-	-0.87	-	-		
TK2233	Hypothetical protein, conserved, DUF437 famil	-0.77	-0.71	-0.74	0.04	-0.21	-0.03	-0.12	0.13		
TK2234	Hypothetical membrane protein, conserved_CO	-1.11	-0.80	-0.95	0.22	-1.08	0.32	-0.38	0.99		
TK2235	Phosphoribosylpyrophosphate synthetase_COG	-1.03	-0.80	-0.91	0.16	-0.21	-0.90	-0.55	0.49		
TK2236	Hypothetical protein, conserved_COG4996	0.31	0.14	0.22	0.12	0.77	-0.26	0.26	0.73	coding	
TK2237	Hypothetical protein, conserved, DUF366 famil	0.56	0.44	0.50	0.08	-1.00	-0.07	-0.54	0.66		
TK2238	Hypothetical membrane protein, conserved	0.61	0.66	0.64	0.03	0.51	0.57	0.54	0.05		
TK2239	PhoI-related type II restriction endonuclease	5.17	5.83	5.50	0.46	2.50	1.75	2.12	0.53	5' (+12)	
TK2240	Lysyl-tRNA synthetase_COG1384	0.58	0.42	0.50	0.12	-0.59	0.18	-0.20	0.55	coding	
TK2241	SAM-dependent methyltransferase, UbiE/COQ	0.20	0.12	0.16	0.06	-0.77	-0.74	-0.75	0.02		
TK2242	GHMP kinase_COG1907	-0.20	-0.23	-0.21	0.03	-0.29	-1.21	-0.75	0.66	coding	
TK2243	Hypothetical protein, conserved, DUF1464 fam	0.30	0.01	0.15	0.20	-0.43	-0.39	-0.41	0.03	coding	
TK2244	Indolepyruvate: ferredoxin oxidoreductase, beta	0.49	0.01	0.25	0.34	-1.01	-1.31	-1.16	0.21		
TK2245	Transcription regulator, SpoVT/AbrB family, co	0.23	0.09	0.16	0.10	-0.47	0.71	0.12	0.83		
TK2246	L-Asparaginase_COG1446	-0.38	0.23	-0.07	0.43	-0.71	-0.30	-0.51	0.29		
TK2247	Predicted permease, major facilitator superfam	0.41	0.33	0.37	0.06	1.80	-	-	-		
TK2248	Biotin synthase-related protein, radical SAM su	0.21	0.16	0.19	0.04	0.58	1.65	1.12	0.76		
TK2249	Hypothetical protein, conserved, containing TP	0.01	0.13	0.07	0.09	-0.59	1.09	0.25	1.19		
TK2250	Serine/threonine protein kinase, RIO1 family_C	0.02	-0.06	-0.02	0.06	-1.28	-0.81	-1.04	0.33		
TK2251	Permease, major facilitator superfamily_COG04	0.05	-0.27	-0.11	0.23	2.49	0.03	1.26	1.74		
TK2252	Proteasome-activating nucleotidase (proteaso	0.13	0.03	0.08	0.07	-0.30	-0.54	-0.42	0.17	coding	
TK2253	Hypothetical protein, conserved, RAMP superfa	0.01	0.06	0.04	0.03	-	0.15	-	-		
TK2254	UDP-N-acetylglucosamine--dolichyl-phosphat	-0.26	-0.09	-0.17	0.12	-	-1.99	-	-		
TK2255	Bifunctional phosphatase/dolichol-phosphate g	0.39	-0.03	0.18	0.29	-	2.53	-	-	coding	
TK2256	Hypothetical membrane protein, conserved_CO	0.15	0.09	0.12	0.05	-0.03	-0.17	-0.10	0.10		coding
TK2257	Deoxycytidylate deaminase_COG2131	0.59	0.32	0.45	0.19	-0.55	-0.31	-0.43	0.17		
TK2258	Zinc-dependent protease HtpX homolog, M48 f	-0.08	-0.01	-0.05	0.05	0.82	-0.06	0.38	0.62		
TK2259	Predicted transcription regulator, penicillinase	-0.39	-0.23	-0.31	0.11	-0.33	-0.36	-0.35	0.02		
TK2260	Dihydroorotate dehydrogenase_COG0167	-0.38	-0.07	-0.23	0.21	-	-0.50	-	-		
TK2261	Transcription regulator, SpoVT/AbrB family_C	-0.12	0.05	-0.03	0.12	-	2.71	-	-		
TK2262	Predicted nucleic acid-binding protein, containi	0.44	0.21	0.33	0.16	0.90	-	-	-		
TK2263	Predicted transcription regulator, ExsB family_C	0.34	-0.04	0.15	0.27	-	-	-	-		
TK2264	Predicted calcium-binding protein_COG1800	2.85	2.68	2.77	0.13	-0.08	-0.21	-0.15	0.09		
TK2265	Hypothetical membrane protein	0.15	-0.10	0.03	0.17	0.74	-0.74	0.00	1.04		
TK2266	Predicted permease, major facilitator superfam	-0.18	-0.16	-0.17	0.02	-0.09	-0.46	-0.28	0.26	coding	
TK2267	Hypothetical membrane protein, conserved, UP	-0.16	-0.07	-0.12	0.06	-0.53	-0.74	-0.64	0.14		
TK2268	Aspartate aminotransferase_COG0436	-0.31	-0.10	-0.20	0.15	-1.18	-1.20	-1.19	0.02		
TK2269	Hypothetical protein, conserved, DUF509 famil	0.00	-0.11	-0.05	0.08	-	2.18	-	-		

TK2270	Hypothetical protein, conserved_COG3609	-0.43	-0.26	-0.34	0.12	-1.12	-1.31	-1.21	0.13		
TK2271	Cell division GTPase_COG0206	-0.43	-0.55	-0.49	0.09	-0.12	-0.59	-0.36	0.34		
TK2272	ATPase involved in chromosome partitioning, P	-0.25	-0.28	-0.26	0.03	-0.50	-0.42	-0.46	0.06		
TK2273	Predicted transcription regulator, CopG/RepA	0.15	-0.17	-0.01	0.22	-1.37	-0.33	-0.85	0.73		
TK2274	Glycerol-3-phosphate cytidylyltransferase_CO	0.27	0.05	0.16	0.16	-0.34	-0.05	-0.20	0.20		
TK2275	RNA-binding protein, containing PUA domain_C	0.12	-0.09	0.01	0.15	-0.03	-1.49	-0.76	1.03		
TK2276	Orotidine-5'-phosphate decarboxylase_COG02	-	-	-	-	-	-	-	-		
TK2277	Hypothetical protein, conserved	-0.23	-0.46	-0.35	0.17	-	-1.06	-	-		
TK2278	myo-Inositol-1-phosphate synthase_COG1260	-1.18	-1.18	-1.18	0.01	-0.52	-0.42	-0.47	0.07	coding	
TK2279	Bifunctional sugar nucleotidyltransferase/CDP	-0.11	-0.15	-0.13	0.02	-	0.75	-	-	coding	coding
TK2280	ATP-binding protein_COG2102	-0.45	-0.27	-0.36	0.13	0.03	1.30	0.67	0.89		
TK2281	ABC-type multidrug transport system, ATPase	1.16	1.36	1.26	0.14	0.57	-	-	-		coding
TK2282	Hypothetical membrane protein, conserved_CO	0.92	0.87	0.89	0.03	-0.06	-0.75	-0.40	0.49		
TK2283	Hypothetical protein, conserved, DUF498 famil	0.51	0.50	0.51	0.01	-	0.21	-	-	coding	
TK2284	Probable 8-oxo-dGTPase, MutT homolog, NUD	0.44	0.24	0.34	0.14	-	0.31	-	-		
TK2285	Carbohydrate/pyrimidine kinase, PfkB family_C	-0.03	-0.15	-0.09	0.08	-	1.33	-	-		
TK2286	snoRNP component, Gar1 homolog_COG3277	-0.13	-0.36	-0.25	0.16	-	0.54	-	-		
TK2287	Transcription initiation factor IIB_COG1405	-0.25	-0.35	-0.30	0.07	0.07	-0.23	-0.08	0.21		
TK2288	Metallophosphoesterase, calcineurin superfamil	-	-0.60	-	-	-0.10	-1.42	-0.76	0.93		
TK2289	Archaeal histone B_COG2036	0.60	0.18	0.39	0.30	-0.80	-0.66	-0.73	0.10		
TK2290	Ribulose 1,5-bisphosphate carboxylase/oxygen	-0.65	-0.61	-0.63	0.02	-1.40	-	-	-	coding	coding
TK2291	Archaeal heat shock regulator, ArsR family_CO	0.03	-0.04	0.00	0.05	-	1.43	-	-		
TK2292	SSU ribosomal protein S17E_COG1383	0.90	0.33	0.62	0.40	-	-	-	-		
TK2293	Hypothetical protein, conserved, DUF371 famil	-0.62	-0.26	-0.44	0.25	-0.23	0.26	0.01	0.35		
TK2294	Hypothetical protein, conserved, UPF0128 fami	0.22	0.12	0.17	0.07	-0.42	0.96	0.27	0.98		
TK2295	Hypothetical membrane protein	-0.51	-0.33	-0.42	0.13	1.45	0.41	0.93	0.73		
TK2296	Hypothetical protein, conserved, radical SAM s	0.19	0.02	0.11	0.12	-	-	-	-		
TK2297	Hypothetical protein, conserved, containing TP	-0.81	-0.24	-0.52	0.40	-	-0.47	-	-		
TK2298	Anaerobic ribonucleoside-triphosphate reducta	0.50	0.37	0.44	0.09	-	-2.14	-	-	coding	
TK2299	Anaerobic ribonucleoside-triphosphate reducta	0.36	0.19	0.27	0.12	-1.56	-1.66	-1.61	0.07	coding	
TK2300	Peptidyl-tRNA hydrolase_COG1990	0.10	-0.14	-0.02	0.17	-	-0.97	-	-		
TK2301	Hydrolase, HAD superfamily_COG0561	0.49	0.27	0.38	0.16	0.82	-0.08	0.37	0.63		
TK2302	tRNA pseudouridine synthase D_COG0585	0.60	0.43	0.51	0.12	0.66	-0.58	0.04	0.88		
TK2303	Chaperonin, beta subunit (thermosome, beta su	-0.01	-0.27	-0.14	0.19	-1.53	-1.61	-1.57	0.06	coding	coding
TK2304	tRNA/rRNA cytosine-C5-methylase, NOL1/NO	0.32	0.17	0.25	0.11	0.38	-0.69	-0.15	0.76		
TK2305	Hypothetical protein, containing leucine zipper	-0.77	-0.89	-0.83	0.08	-	-1.14	-	-		
TK2306	Predicted nucleic acid-binding protein, contain	-0.05	-0.33	-0.19	0.20	-	-	-	-		

Appendix D. Distribution of TrmB family proteins among the three domains

Numbers of predicted proteins with TrmB and/or Regulator_TrmB domains in each species are indicated. The list of organisms derives from the KEGG database; the list of proteins that possess TrmB and/or Regulator_TrmB domains derives from the Pfam database.

Appendix D. Distribution of proteins that possess TrmB and/or Regulator_TrmB domains

Eukaryotes					Number of proteins with followin domains		
Category			Species		TrmB	Regulator_TrmB	Both
Animals	Vertebrate	Mammals	hsa	Homo sapiens (human)			
			ptr	Pan troglodytes (chimpanzee)			
			mcc	Macaca mulatta (rhesus monkey)			
			mmu	Mus musculus (mouse)			
			rno	Rattus norvegicus (rat)			
			cfa	Canis familiaris (dog)			
			bta	Bos taurus (cow)			
			ssc	Sus scrofa (pig)			
			ecb	Equus caballus (horse)			
			mdo	Monodelphis domestica (opossum)			
			oaa	Ornithorhynchus anatinus (platypus)			
		Birds	gga	Gallus gallus (chicken)			
			tgu	Taeniopygia guttata (zebra finch)			
		Amphibians	xla	Xenopus laevis (African clawed frog)			
			xtr	Xenopus tropicalis (western clawed frog)			
		Fishes	dre	Danio rerio (zebrafish)			
			dfru	Fugu rubripes (Japanese puffer fish)			
			dtni	Tetraodon nigroviridis (green spotted puffer)			
			dola	Oryzias latipes (Japanese medaka)			
	Lancelets		bfo	Branchiostoma floridae (Florida lancelet)			
	Ascidians		cin	Ciona intestinalis (sea squirt)			
	Echinoderms		spu	Strongylocentrotus purpuratus (purple sea urchin)			
	Arthropod	Insects	dme	Drosophila melanogaster (fruit fly)			
			dpo	Drosophila pseudoobscura pseudoobscura			
			dan	Drosophila ananassae			
			der	Drosophila erecta			
			dpe	Drosophila persimilis			
			dse	Drosophila sechellia			
			dsi	Drosophila simulans			
			dwi	Drosophila willistoni			
			dya	Drosophila yakuba			
			dgr	Drosophila grimshawi			
			dmo	Drosophila mojavensis			
			dvi	Drosophila virilis			
			aga	Anopheles gambiae (mosquito)			
			aag	Aedes aegypti (yellow fever mosquito)			
			cqu	Culex quinquefasciatus (southern house mosquito)			
			ame	Apis mellifera (honey bee)			
			nvi	Nasonia vitripennis (jewel wasp)			
			dbmo	Bombyx mori (silkmoth)			
			tca	Tribolium castaneum (red flour beetle)			
			api	Acyrthosiphon pisum (pea aphid)			
			dapi	Acyrthosiphon pisum (pea aphid) (AphidBase)			
			dphu	Pediculus humanus (human body louse)			
		Mites and ticks	isc	Ixodes scapularis (black-legged tick)			
	Nematodes		cel	Caenorhabditis elegans (nematode)			
			cbr	Caenorhabditis briggsae		1	
			bmy	Brugia malayi (filaria)			
	Flatworms		smm	Schistosoma mansoni			
	Cnidarians		nve	Nematostella vectensis (sea anemone)			
			hmg	Hydra magnipapillata			
	Placozoans		tad	Trichoplax adhaerens			
Plants	Eudicots	Mustard family	ath	Arabidopsis thaliana (thale cress)			
		Willow family	pop	Populus trichocarpa (black cottonwood)			
		Spurge family	rcu	Ricinus communis (castor bean)			
		Grape family	vvi	Vitis vinifera (wine grape)			
	Monocots	Grass family	osa	Oryza sativa japonica (Japanese rice)			
			dosa	Oryza sativa japonica (Japanese rice) (RAPDB)			
			sbi	Sorghum bicolor (sorghum)			
			zma	Zea mays (maize)			
	Mosses		ppp	Physcomitrella patens subsp. patens			
	Green algae		cre	Chlamydomonas reinhardtii			
			olu	Ostreococcus lucimarinus			
			dota	Ostreococcus tauri			
	Red algae		cme	Cyanidioschyzon merolae			
Fungi	Ascomyce	Saccharomycetes	sce	Saccharomyces cerevisiae (budding yeast)			
			dsrd	Saccharomyces paradoxus			
			dsmi	Saccharomyces mikatae			
			dsba	Saccharomyces bayanus			
			ago	Ashbya gossypii (Eremothecium gossypii)			
			kla	Kluyveromyces lactis			
			lth	Lachancea thermotolerans			
			dkwa	Kluyveromyces waltii			
			dha	Debaryomyces hansenii			
			pic	Pichia stipitis			
			ppa	Pichia pastoris			
			pgu	Pichia guilliermondii			
			vpo	Vanderwaltozyma polyspora			
			lel	Lodderomyces elongisporus			
			zro	Zygosaccharomyces rouxii			
			cal	Candida albicans			
			ctp	Candida tropicalis			
			cdu	Candida dubliniensis			
			cgr	Candida glabrata			
			yli	Yarrowia lipolytica			
			clu	Clavispora lusitaniae			
		Schizosaccharomyce	spo	Schizosaccharomyces pombe (fission yeast)			

		Sordariomycetes	ncr	Neurospora crassa	
			pan	Podospora anserina	
			mgr	Magnaporthe grisea	
			fgr	Fusarium graminearum	
		Eurotiomycetes	ani	Aspergillus nidulans	
			afm	Aspergillus fumigatus	
			aor	Aspergillus oryzae	
			ang	Aspergillus niger	
			afv	Aspergillus flavus	
			act	Aspergillus clavatus	
			pcs	Penicillium chrysogenum	
			nfi	Neosartorya fischeri	
			cim	Coccidioides immitis	
			ure	Uncinocarpus reesii	
		Leotiomycetes	ssl	Sclerotinia sclerotiorum	
			bfu	Botryotinia fuckeliana	
		Dothideomycetes	pno	Phaeosphaeria nodorum	
	Basidiomycetes		cne	Cryptococcus neoformans JEC21	
			cnb	Cryptococcus neoformans B-3501A	
			ppl	Postia placenta	
			dpch	Phanerochaete chrysosporium	
			lbc	Laccaria bicolor	
			mpr	Moniliophthora perniciosa	
			uma	Ustilago maydis	
			mgl	Malassezia globosa	
	Microsporidians		ecu	Encephalitozoon cuniculi	
Protists	Choanoflagellates		mbr	Monosiga brevicollis	
	Amoebozo	Dictyostelium	ddi	Dictyostelium discoideum (cellular slime mold)	
		Entamoeba	ehi	Entamoeba histolytica	
			edi	Entamoeba dispar	
	Alveolates	Apicomplexans	pfa	Plasmodium falciparum 3D7	
			pfd	Plasmodium falciparum Dd2	
			pfh	Plasmodium falciparum HB3	
			pyo	Plasmodium yoelii	
			pcb	Plasmodium chabaudi	
			pbe	Plasmodium berghei	
			pkn	Plasmodium knowlesi	
			pvx	Plasmodium vivax	
			tan	Theileria annulata	
			tpv	Theileria parva	
			bbo	Babesia bovis	1
			cpv	Cryptosporidium parvum	
			cho	Cryptosporidium hominis	
			tgo	Toxoplasma gondii	
		Ciliates	tet	Tetrahymena thermophila	
			ptm	Paramecium tetraurelia	
	Euglenozo	Kinetoplasts	tbr	Trypanosoma brucei	
			tcr	Trypanosoma cruzi	
			lma	Leishmania major	
			lif	Leishmania infantum	
			lbz	Leishmania braziliensis	
	Diplomonads		gla	Giardia lamblia	
	Parabasalids		tva	Trichomonas vaginalis	
	Diatoms		pti	Phaeodactylum tricornutum	
			tps	Thalassiosira pseudonana	

Prokaryotes

Category			Species		
Bacteria	Gammaprd	Escherichia	eco	Escherichia coli K-12 MG1655	
			ecj	Escherichia coli K-12 W3110	
			ecd	Escherichia coli K-12 DH10B	
			ebw	Escherichia coli K-12 MC4100(MuLac) BW2952	
			ece	Escherichia coli O157:H7 EDL933 (EHEC)	
			ecs	Escherichia coli O157:H7 Sakai (EHEC)	
			ecf	Escherichia coli O157:H7 EC4115 (EHEC)	
			etw	Escherichia coli O157:H7 TW14359 (EHEC)	
			ecg	Escherichia coli O127:H6 (EPEC)	
			ecc	Escherichia coli O6:H1 CFT073 (UPEC)	
			eci	Escherichia coli UTI89 (UPEC)	
			ecp	Escherichia coli 536 (UPEC)	
			ecv	Escherichia coli O1 (APEC)	
			ecw	Escherichia coli O139:H28 E24377A (ETEC)	
			ecx	Escherichia coli O9 HS (commensal)	
			ecm	Escherichia coli SECEC	
			ecy	Escherichia coli O152:H28 SE11 (commensal)	
			ecl	Escherichia coli ATCC 8739	
			eck	Escherichia coli 55989 (EAEC)	
			ecq	Escherichia coli ED1a	
			ecr	Escherichia coli IAI1 (commensal)	
			ect	Escherichia coli O7:K1 IAI39 (ExPEC)	
			ecz	Escherichia coli O45:K1 S88 (ExPEC)	
			eum	Escherichia coli O17:K52:H18 UMN026 (ExPEC)	
			elf	Escherichia coli LF82	
			ebl	Escherichia coli BL21	
			ebd	Escherichia coli BL21(DE3)	
			ebr	Escherichia coli B REL606	
			eoh	Escherichia coli O103:H2 12009	
			eoi	Escherichia coli O111:H- 11128	1
			eoj	Escherichia coli O26:H11 11368	1
			eok	Escherichia coli O55:H7 CB9615	
			efe	Escherichia fergusonii	
		Salmonella	sty	Salmonella enterica subsp. enterica serovar Typhi CT18	

			stt	Salmonella enterica subsp. enterica serovar Typhi Ty2		
			stm	Salmonella enterica subsp. enterica serovar Typhimurium LT2		
			spt	Salmonella enterica subsp. enterica serovar Paratyphi A ATCC9150		
			sek	Salmonella enterica subsp. enterica serovar Paratyphi A AKU12601		
			spq	Salmonella enterica subsp. enterica serovar Paratyphi B		
			sei	Salmonella enterica subsp. enterica serovar Paratyphi C		
			sec	Salmonella enterica subsp. enterica serovar Choleraesuis		
			seh	Salmonella enterica subsp. enterica serovar Heidelberg		
			see	Salmonella enterica subsp. enterica serovar Newport		
			sew	Salmonella enterica subsp. enterica serovar Schwarzengrund		
			sea	Salmonella enterica subsp. enterica serovar Agona		
			sed	Salmonella enterica subsp. enterica serovar Dublin		
			seg	Salmonella enterica subsp. enterica serovar Gallinarum		
			set	Salmonella enterica subsp. enterica serovar Enteritidis		
			ses	Salmonella enterica subsp. arizonae		
		Yersinia	ype	Yersinia pestis CO92 (biovar Orientalis)		
			ypk	Yersinia pestis KIM (biovar Mediaevalis)		
			ypm	Yersinia pestis Mediaevails (biovar Mediaevalis)		
			ypa	Yersinia pestis Antiqua (biovar Antiqua)		
			ypn	Yersinia pestis Nepal516 (biovar Antiqua)		
			ypg	Yersinia pestis Angola (biovar Antiqua)		
			ypp	Yersinia pestis Pestoides (biovar Microtus)		
			ypz	Yersinia pestis Z176003		
			yps	Yersinia pseudotuberculosis IP32953		1
			ypi	Yersinia pseudotuberculosis IP31758		1
			ypy	Yersinia pseudotuberculosis YPIII		
			ypb	Yersinia pseudotuberculosis PB1/+		
			yen	Yersinia enterocolitica		1
		Shigella	sfl	Shigella flexneri 301 (serotype 2a)		
			sfx	Shigella flexneri 2457T (serotype 2a)		
			sfv	Shigella flexneri 8401 (serotype 5b)		
			ssn	Shigella sonnei		
			sbo	Shigella boydii Sb227		
			sbc	Shigella boydii CDC 3083-94		
			sdy	Shigella dysenteriae		
		Pectobacterium	eca	Erwinia carotovora		
			pct	Pectobacterium carotovorum		
			pwa	Pectobacterium wasabiae		
		Erwinia	eta	Erwinia tasmaniensis		
			epy	Erwinia pyrifoliae		
			eam	Erwinia amylovora		1
			eay	Erwinia amylovora ATCC 49946		1
		Photorhabdus	plu	Photorhabdus luminescens		
			pay	Photorhabdus asymbiotica		
		Buchnera	buc	Buchnera aphidicola APS		
			bas	Buchnera aphidicola Sg		
			bab	Buchnera aphidicola Bp		
			bcc	Buchnera aphidicola Cc		
			bap	Buchnera aphidicola 5A		
			bau	Buchnera aphidicola Tuc7		
		Wigglesworthia	wbr	Wigglesworthia glossinidia		
		Sodalis	sgl	Sodalis glossinidius		
		Enterobacter	ent	Enterobacter sp. 638		
		Cronobacter	esa	Enterobacter sakazakii		
			ctu	Cronobacter turicensis		
		Klebsiella	kpn	Klebsiella pneumoniae		1
			kpe	Klebsiella pneumoniae 342		
			kpu	Klebsiella pneumoniae NTUH-K2044		
			kva	Klebsiella variicola		
		Citrobacter	cko	Citrobacter koseri ATCC BAA-895		
			cro	Citrobacter rodentium		
		Serratia	spe	Serratia proteamaculans		
		Proteus	pmr	Proteus mirabilis		
		Edwardsiella	eic	Edwardsiella ictaluri		
			etr	Edwardsiella tarda		
		Blochmannia	bfl	Candidatus Blochmannia floridanus		
			bpn	Candidatus Blochmannia pennsylvanicus		
		Hamiltonella	hde	Candidatus Hamiltonella defensa		
		Dickeya	dda	Dickeya dadantii Ech703		
			ddc	Dickeya dadantii Ech586		
			dze	Dickeya zeae		
		Xenorhabdus	xbo	Xenorhabdus bovienii		
		Pantoea	pam	Pantoea ananatis		
		Haemophilus	hin	Haemophilus influenzae Rd KW20 (serotype d)		
			hit	Haemophilus influenzae 86-028NP (nontypeable)		
			hip	Haemophilus influenzae PittEE		
			hiq	Haemophilus influenzae PittGG		
			hdu	Haemophilus ducreyi		
			hap	Haemophilus parasuis		
		Histophilus	hso	Haemophilus somnus 129PT		
			hsm	Haemophilus somnus 2336		
		Pasteurella	pmu	Pasteurella multocida		
		Mannheimia	msu	Mannheimia succiniciproducens		
		Actinobacillus	apl	Actinobacillus pleuropneumoniae L20 (serotype 5b)		
			apj	Actinobacillus pleuropneumoniae JL03 (serotype 3)		
			apa	Actinobacillus pleuropneumoniae AP76 (serotype 7)		
			asu	Actinobacillus succinogenes	1	
		Aggregatibacter	aap	Aggregatibacter aphrophilus		
			aat	Aggregatibacter actinomycetemcomitans		
		Xylella	xfa	Xylella fastidiosa 9a5c		
			xft	Xylella fastidiosa Temecula1		
			xfm	Xylella fastidiosa M12		
			xfn	Xylella fastidiosa M23		

Xanthomonas	xcc	Xanthomonas campestris pv. campestris ATCC 33913			
	xcb	Xanthomonas campestris pv. campestris 8004			
	xca	Xanthomonas campestris pv. campestris B100			
	xcv	Xanthomonas campestris pv. vesicatoria			
	xac	Xanthomonas axonopodis			
	xoo	Xanthomonas oryzae KACC10331			
	xom	Xanthomonas oryzae MAFF311018			
	xop	Xanthomonas oryzae PXO99A			
	xal	Xanthomonas albilineans			
Stenotrophomonas	sml	Stenotrophomonas maltophilia K279a			
	smt	Stenotrophomonas maltophilia R551-3			
Vibrio	vch	Vibrio cholerae O1	1	1	1
	vco	Vibrio cholerae O395	1	1	1
	vcm	Vibrio cholerae M66-2	1	1	1
	vcj	Vibrio cholerae MJ-1236	1	1	1
	vvu	Vibrio vulnificus CMCP6		2	
	vvy	Vibrio vulnificus YJ016		2	
	vpa	Vibrio parahaemolyticus	2	2	
	vha	Vibrio harveyi	2	1	
	vsp	Vibrio splendidus	2	1	1
	vex	Vibrio sp. Ex25	1	1	
Aliivibrio	vfi	Vibrio fischeri			
	vfm	Vibrio fischeri MJ11	2	1	
	vsa	Aliivibrio salmonicida LFI1238			
Photobacterium	ppr	Photobacterium profundum			
Pseudomonas	pae	Pseudomonas aeruginosa PAO1	1		
	pau	Pseudomonas aeruginosa UCBPP-PA14	1		
	pap	Pseudomonas aeruginosa PA7	1		
	pag	Pseudomonas aeruginosa LESB58	1		
	ppu	Pseudomonas putida KT2440	1		
	ppf	Pseudomonas putida F1	1		
	ppg	Pseudomonas putida GB-1	1		
	ppw	Pseudomonas putida W619	1		
	pst	Pseudomonas syringae pv. tomato DC3000			
	psb	Pseudomonas syringae pv. syringae B728a			
	psp	Pseudomonas syringae pv. phaseolicola 1448A			
	pfl	Pseudomonas fluorescens Pf-5	1		
	pfo	Pseudomonas fluorescens Pf0-1	1		
	pfs	Pseudomonas fluorescens SBW25	1		
	pen	Pseudomonas entomophila	1		
	pmy	Pseudomonas mendocina			
	psa	Pseudomonas stutzeri			
Cellvibrio	cja	Cellvibrio japonicus			
Azotobacter	avn	Azotobacter vinelandii	1		
Psychrobacter	par	Psychrobacter arcticum	1		
	pcr	Psychrobacter cryohalolentis	1		
	prw	Psychrobacter sp. PRwf-1			
Acinetobacter	aci	Acinetobacter sp. ADP1			
	acb	Acinetobacter baumannii ATCC 17978			
	abm	Acinetobacter baumannii SDF			
	aby	Acinetobacter baumannii AYE			
	abc	Acinetobacter baumannii ACICU			
	abn	Acinetobacter baumannii AB0057			
	abb	Acinetobacter baumannii AB307-0294			
Shewanella	son	Shewanella oneidensis			
	sdn	Shewanella denitrificans			
	sfr	Shewanella frigidimarina			
	saz	Shewanella amazonensis			
	sbl	Shewanella baltica OS155			
	sbm	Shewanella baltica OS185			
	sbn	Shewanella baltica OS195			
	sbp	Shewanella baltica OS223			
	slo	Shewanella loihica		1	
	spc	Shewanella putrefaciens			
	sse	Shewanella sediminis			
	spl	Shewanella pealeana			
	she	Shewanella sp. MR-4			
	shm	Shewanella sp. MR-7			
	shn	Shewanella sp. ANA-3			
	shw	Shewanella sp. W3-18-1	1		
	shl	Shewanella halifaxensis			
	swd	Shewanella woodyi ATCC 51908			
	swp	Shewanella piezotolerans WP3			
	svo	Shewanella violacea			
Idiomarina	ilo	Idiomarina loihiensis			
Colwellia	cps	Colwellia psychrerythraea	2		
Pseudoalteromonas	pha	Pseudoalteromonas haloplanktis			
	pat	Pseudoalteromonas atlantica			
Saccharophagus	sde	Saccharophagus degradans			
Marinobacter	maq	Marinobacter aquaeolei			
Alteromonas	amc	Alteromonas macleodii	1		
Psychromonas	pin	Psychromonas ingrahamii			
Teredinibacter	ttu	Teredinibacter turnerae			
Coxiella	cbu	Coxiella burnetii RSA 493			
	cbs	Coxiella burnetii RSA 331			
	cbd	Coxiella burnetii Dugway 5J108-111			
	cbg	Coxiella burnetii CbuG_Q212		1	
	cbc	Coxiella burnetii CbuK_Q154			
Legionella	lpn	Legionella pneumophila Philadelphia 1			
	lpf	Legionella pneumophila Lens			
	lpp	Legionella pneumophila Paris			
	lpc	Legionella pneumophila Corby			
	llo	Legionella longbeachae			

		Methylococcus	mca	Methylococcus capsulatus			
		Francisella	ftu	Francisella tularensis subsp. tularensis SCHU S4			
			ftf	Francisella tularensis subsp. tularensis FSC 198			
			ftw	Francisella tularensis subsp. tularensis WY96-3418			
			ftl	Francisella tularensis subsp. holarctica LVS			
			fth	Francisella tularensis subsp. holarctica OSU18			
			fta	Francisella tularensis subsp. holarctica FTNF002-00			
			ftm	Francisella tularensis subsp. mediasiatica FSC147			
			ftn	Francisella novicida U112			
			fph	Francisella philomiragia			
		Thiomicrospira	tcx	Thiomicrospira crunogena	1		
		Nitrosococcus	noc	Nitrosococcus oceani			
			nhl	Nitrosococcus halophilus			
		Allochromatium	alv	Allochromatium vinosum			
		Alkalilimnicola	aeh	Alkalilimnicola ehrlichei			
		Halorhodospira	hha	Halorhodospira halophila			
		Thioalkalivibrio	tgr	Thioalkalivibrio sp. HL-EbGR7	1		
			tkm	Thioalkalivibrio sp. K90mix			
		Halothiobacillus	hna	Halothiobacillus neapolitanus			
		Hahella	hch	Hahella chejuensis			
		Chromohalobacter	csa	Chromohalobacter salexigens			
		Alcanivorax	abo	Alcanivorax borkumensis			
		Marinomonas	mmw	Marinomonas sp. MWYL1	1		
		Aeromonas	aha	Aeromonas hydrophila			
			asa	Aeromonas salmonicida			
		Tolumonas	tau	Tolumonas auensis			
		Dichelobacter	dno	Dichelobacter nodosus			
		Acidithiobacillus	afe	Acidithiobacillus ferrooxidans ATCC 53993			
			afr	Acidithiobacillus ferrooxidans ATCC 23270			
		Baumannia	bci	Baumannia cicadellinicola			
		Carsonella	crp	Candidatus Carsonella ruddii			
		Ruthia	rma	Candidatus Ruthia magnifica			
		Vesicomyosocius	vok	Candidatus Vesicomyosocius okutanii			
		Kangiella	kko	Kangiella koreensis			
	Betaprote	Neisseria	nma	Neisseria meningitidis Z2491 (serogroup A)			
			nme	Neisseria meningitidis MC58 (serogroup B)			
			nmc	Neisseria meningitidis FAM18 (serogroup C)			
			nmn	Neisseria meningitidis 053442 (serogroup C)			
			nmi	Neisseria meningitidis alpha14			
			ngo	Neisseria gonorrhoeae FA 1090			
			ngk	Neisseria gonorrhoeae NCCP11945			
		Chromobacterium	cvi	Chromobacterium violaceum			
		Laribacter	lhk	Laribacter hongkongensis			
		Ralstonia	rso	Ralstonia solanacearum			
			rpi	Ralstonia pickettii 12J	1		
			rpf	Ralstonia pickettii 12D	1		
		Cupriavidus	reu	Ralstonia eutropha JMP134	1	1	1
			reh	Ralstonia eutropha H16	1		
			rme	Ralstonia metallidurans	1		
			cti	Cupriavidus taiwanensis	1		
		Burkholderia	bma	Burkholderia mallei ATCC 23344			
			bmv	Burkholderia mallei SAVP1			
			bml	Burkholderia mallei NCTC 10229			
			bmn	Burkholderia mallei NCTC 10247			
			bps	Burkholderia pseudomallei K96243			
			bpm	Burkholderia pseudomallei 1710b			
			bpl	Burkholderia pseudomallei 1106a			
			bpd	Burkholderia pseudomallei 668			
			bpr	Burkholderia pseudomallei MSHR346			
			bte	Burkholderia thailandensis			
			bvi	Burkholderia vietnamiensis	1	1	1
			bur	Burkholderia sp. 383	1	1	1
			bcn	Burkholderia cenocepacia AU1054	1	1	1
			bch	Burkholderia cenocepacia HI2424	1	1	1
			bcm	Burkholderia cenocepacia MC0-3	1		
			bcj	Burkholderia cenocepacia J2315	1		
			bam	Burkholderia cepacia			
			bac	Burkholderia ambifaria MC40-6			
			bmu	Burkholderia multivorans ATCC 17616 (JGI)	2		
			bmj	Burkholderia multivorans ATCC 17616 (Tohoku)	2		
			bxe	Burkholderia xenovorans			
			bph	Burkholderia phymatum			
			bpy	Burkholderia phytofirmans			
			bgl	Burkholderia glumae			
		Polynucleobacter	pnu	Polynucleobacter sp. QLW-P1DMWA-1	1		
			pne	Polynucleobacter necessarius			
		Bordetella	bpe	Bordetella pertussis	1	1	1
			bpa	Bordetella parapertussis	1	1	1
			bbr	Bordetella bronchiseptica	1	1	1
			bpt	Bordetella petrii	2		
			bav	Bordetella avium			
		Rhodoferax	rfr	Rhodoferax ferrireducens			
		Polaromonas	pol	Polaromonas sp. JS666			
			pna	Polaromonas naphthalenivorans			
		Acidovorax	aav	Acidovorax avenae			
			ajs	Acidovorax sp. JS42	2		
			dia	Acidovorax ebreus			
		Verminephrobacter	vei	Verminephrobacter eiseniae			
		Delftia	dac	Delftia acidovorans	1		
		Variovorax	vap	Variovorax paradoxus	2		
		Comamonas	ctt	Comamonas testosteroni			
		Methylibium	mpt	Methylibium petroleiphilum	2		
		Herminiimonas	har	Herminiimonas arsenicoxydans	1		

		Minibacterium	mms	Minibacterium massiliensis				
		Leptothrix	lch	Leptothrix cholodnii				
		Nitrosomonas	neu	Nitrosomonas europaea				
			net	Nitrosomonas eutropha				
		Nitrosospira	nmu	Nitrosospira multiformis				
		Aromatoleum	eba	Aromatoleum aromaticum EbN1				
		Azoarcus	azo	Azoarcus sp. BH72	1			
		Dechloromonas	dar	Dechloromonas aromatica				
		Thauera	tmz	Thauera sp. MZ1T				
		Thiobacillus	tbd	Thiobacillus denitrificans				
		Methylobacillus	mfa	Methylobacillus flagellatus				
		Methylotenera	mmb	Methylotenera mobilis				
		Methylovorus	mei	Methylovorus sp. SIP3-4				
		Accumulibacter	app	Accumulibacter phosphatis				
		Sideroxydans	slt	Sideroxydans lithotrophicus				
	Epsilonpro	Helicobacter	hpy	Helicobacter pylori 26695				
			hpj	Helicobacter pylori J99				
			hpa	Helicobacter pylori HPAG1				
			hps	Helicobacter pylori Shi470				
			hpg	Helicobacter pylori G27				
			hpp	Helicobacter pylori P12				
			hpb	Helicobacter pylori B38				
			hhe	Helicobacter hepaticus		1		
			hac	Helicobacter acinonychis	1			
			hms	Helicobacter mustelae				
		Wolinella	wsu	Wolinella succinogenes				
		Sulfurimonas	tdn	Sulfurimonas denitrificans				
		Campylobacter	cje	Campylobacter jejuni NCTC11168				
			cjr	Campylobacter jejuni RM1221				
			cjj	Campylobacter jejuni 81-176				
			cju	Campylobacter jejuni 81116				
			cjd	Campylobacter jejuni subsp. doylei 269.97				
			cff	Campylobacter fetus				
			ccv	Campylobacter curvus				
			cha	Campylobacter hominis ATCC BAA-381				
			cco	Campylobacter concisus 13826				
			cla	Campylobacter lari				
		Arcobacter	abu	Arcobacter butzleri				
		Sulfurospirillum	sdl	Sulfurospirillum deleyianum				
		Nitratiruptor	nis	Nitratiruptor sp. SB155-2		1		
		Sulfurovum	sun	Sulfurovum sp. NBC37-1				
		Nautilia	nam	Nautilia profundicola				
	Deltaprote	Geobacter	gsu	Geobacter sulfurreducens	1			
			gme	Geobacter metallireducens	1			
			gur	Geobacter uraniumreducens				
			glo	Geobacter lovleyi				
			gbm	Geobacter bemidjiensis				
			geo	Geobacter sp. FRC-32	1			
			gem	Geobacter sp. M21	2			
		Pelobacter	pca	Pelobacter carbinolicus	1			
			ppd	Pelobacter propionicus				
		Desulfovibrio	dvu	Desulfovibrio vulgaris Hildenborough	2			
			dvl	Desulfovibrio vulgaris DP4	3			
			dvm	Desulfovibrio vulgaris Miyazaki F	1			
			dde	Desulfovibrio desulfuricans G20	1			
			dds	Desulfovibrio desulfuricans ATCC 27774	1			
			dma	Desulfovibrio magneticus	1			
			dsa	Desulfovibrio salexigens	1			
		Lawsonia	lip	Lawsonia intracellularis				
		Desulfomicrobium	dba	Desulfomicrobium baculatum				
		Desulfohalobium	drt	Desulfohalobium retbaense				
		Bdellovibrio	bba	Bdellovibrio bacteriovorus				
		Desulfotalea	dps	Desulfotalea psychrophila				
		Desulfococcus	dol	Desulfococcus oleovorans				
		Desulfatibacillum	dal	Desulfatibacillum alkenivorans	1			
		Desulfobacterium	dat	Desulfobacterium autotrophicum	2	1		1
		Anaeromyxobacter	ade	Anaeromyxobacter dehalogenans 2CP-C				
			acp	Anaeromyxobacter dehalogenans 2CP-1				
			afw	Anaeromyxobacter sp. Fw109-5				
			ank	Anaeromyxobacter sp. K				
		Myxococcus	mxa	Myxococcus xanthus	1	1		
		Sorangium	scl	Sorangium cellulosum	1			
		Haliangium	hoh	Haliangium ochraceum				
		Syntrophus	sat	Syntrophus aciditrophicus				
		Syntrophobacter	sfu	Syntrophobacter fumaroxidans				
	Alphaprote	Rickettsia	rpr	Rickettsia prowazekii				
			rty	Rickettsia typhi				
			rcm	Rickettsia canadensis				
			rco	Rickettsia conorii				
			rfe	Rickettsia felis				
			rak	Rickettsia akari				
			rri	Rickettsia rickettsii Sheila Smith				
			rrj	Rickettsia rickettsii Iowa				
			rms	Rickettsia massiliae				
			rpk	Rickettsia peacockii				
			raf	Rickettsia africae				
			rbe	Rickettsia bellii RML369-C				
			rbo	Rickettsia bellii OSU 85-389				
		Orientia	ots	Orientia tsutsugamushi Boryong		1		
			ott	Orientia tsutsugamushi Ikeda		1		
		Wolbachia	wol	Wolbachia wMel				
			wbm	Wolbachia wBm				
			wri	Wolbachia sp. wRi				

			wpi	Wolbachia pipientis			
		Anaplasma	ama	Anaplasma marginale St. Maries			
			amf	Anaplasma marginale Florida			
			acn	Anaplasma centrale			
			aph	Anaplasma phagocytophilum			
		Ehrlichia	eru	Ehrlichia ruminantium Welgevonden (South Africa)			
			erw	Ehrlichia ruminantium Welgevonden (France)			
			erg	Ehrlichia ruminantium Gardel			
			ecn	Ehrlichia canis			
			ech	Ehrlichia chaffeensis			
		Neorickettsia	nse	Neorickettsia sennetsu			
			nri	Neorickettsia risticii			
		Pelagibacter	pub	Candidatus Pelagibacter ubique			
		Mesorhizobium	mlo	Mesorhizobium loti			
		Chelativorans	mes	Mesorhizobium sp. BNC1			
		Parvibaculum	pla	Parvibaculum lavamentivorans			
		Sinorhizobium	sme	Sinorhizobium meliloti	2		
			smd	Sinorhizobium medicae			
		Agrobacterium	atu	Agrobacterium tumefaciens C58	1		
			atc	Agrobacterium tumefaciens C58 (Cereon)	1		
			ara	Agrobacterium radiobacter K84	3		
			avi	Agrobacterium vitis S4	2		
		Rhizobium	ret	Rhizobium etli CFN 42			
			rec	Rhizobium etli CIAT 652			
			rle	Rhizobium leguminosarum			
			rlt	Rhizobium leguminosarum bv. trifolii WSM2304			
			rlg	Rhizobium leguminosarum bv. trifolii WSM1325			
			rhi	Rhizobium sp. NGR234			
		Liberibacter	las	Candidatus Liberibacter asiaticus			
		Brucella	bme	Brucella melitensis 16M			
			bmi	Brucella melitensis ATCC 23457			
			bmf	Brucella melitensis biovar Abortus			
			bmb	Brucella abortus 9-941			
			bmc	Brucella abortus S19			
			bms	Brucella suis 1330			
			bmt	Brucella suis ATCC 23445			
			bov	Brucella ovis			
			bcs	Brucella canis			
			bmr	Brucella microti			
		Ochrobactrum	oan	Ochrobactrum anthropi			
		Bradyrhizobium	bja	Bradyrhizobium japonicum			
			bra	Bradyrhizobium sp. ORS278	1		
			bbt	Bradyrhizobium sp. BTAi1	1		
		Rhodopseudomonas	rpa	Rhodopseudomonas palustris CGA009	1		
			rpb	Rhodopseudomonas palustris HaA2	1		
			rpc	Rhodopseudomonas palustris BisB18	1		
			rpd	Rhodopseudomonas palustris BisB5	1		
			rpe	Rhodopseudomonas palustris BisA53	1		
			rpt	Rhodopseudomonas palustris TIE-1	1		
		Nitrobacter	nwi	Nitrobacter winogradskyi			
			nha	Nitrobacter hamburgensis			
		Oligotropha	oca	Oligotropha carboxidovorans			
		Bartonella	bhe	Bartonella henselae			
			bqu	Bartonella quintana			
			bbk	Bartonella bacilliformis			
			btr	Bartonella tribocorum			
			bgr	Bartonella grahamii			
		Xanthobacter	xau	Xanthobacter autotrophicus	2	1	1
		Azorhizobium	azc	Azorhizobium caulinodans			
		Methylobacterium	mex	Methylobacterium extorquens	1		
			mea	Methylobacterium extorquens AM1	1		
			mdi	Methylobacterium extorquens DM4	1		
			mrd	Methylobacterium radiotolerans			
			met	Methylobacterium sp. 4-46			
			mpo	Methylobacterium populi			
			mch	Methylobacterium chloromethanicum			
			mno	Methylobacterium nodulans			
		Beijerinckia	bid	Beijerinckia indica			
		Methylocella	msl	Methylocella silvestris			
		Hodgkinia	hci	Candidatus Hodgkinia cicadicola			
		Caulobacter	ccr	Caulobacter crescentus CB15			
			ccs	Caulobacter crescentus NA1000			
			cak	Caulobacter sp. K31			
		Phenylobacterium	pzu	Phenylobacterium zucineum			
		Ruegeria	sil	Silicibacter pomeroyi	1		
			sit	Silicibacter sp. TM1040	1		
		Rhodobacter	rsp	Rhodobacter sphaeroides 2.4.1	1		
			rsh	Rhodobacter sphaeroides ATCC 17029	1	1	1
			rsq	Rhodobacter sphaeroides ATCC 17025	1		
			rsk	Rhodobacter sphaeroides KD131	1	1	1
			rcp	Rhodobacter capsulatus			
		Jannaschia	jan	Jannaschia sp. CCS1			
		Roseobacter	rde	Roseobacter denitrificans			
		Paracoccus	pde	Paracoccus denitrificans			
		Dinoroseobacter	dsh	Dinoroseobacter shibae			
		Maricaulis	mmr	Maricaulis maris			
		Hyphomonas	hne	Hyphomonas neptunium			
		Hirschia	hba	Hirschia baltica			
		Zymomonas	zmo	Zymomonas mobilis			
			zmn	Zymomonas mobilis subsp. mobilis NCIMB 11163			
		Novosphingobium	nar	Novosphingobium aromaticivorans			
		Sphingopyxis	sal	Sphingopyxis alaskensis			
		Sphingomonas	swi	Sphingomonas wittichii	1		

		Sphingobium	sjp	Sphingobium japonicum			
		Erythrobacter	eli	Erythrobacter litoralis			
		Gluconobacter	gox	Gluconobacter oxydans	1		
		Granulobacter	gbe	Granulobacter bethesdensis			
		Acidiphilium	acr	Acidiphilium cryptum JF-5			
		Gluconacetobacter	gdi	Gluconacetobacter diazotrophicus PAl 5 (Brazil)			
			gdj	Gluconacetobacter diazotrophicus PAl 5 (JGI)			
		Acetobacter	apt	Acetobacter pasteurianus			
		Rhodospirillum	rru	Rhodospirillum rubrum			
			rce	Rhodospirillum centenum	1		
		Magnetospirillum	mag	Magnetospirillum magneticum			
		Azospirillum	azl	Azospirillum sp. B510			
		Unclassified	apb	Alpha proteobacterium IMCC1322			
	Other prot	Magnetococcus	mgm	Magnetococcus sp. MC-1			
	Firmicutes	Bacillus	bsu	Bacillus subtilis	1	1	1
			bha	Bacillus halodurans			
			ban	Bacillus anthracis Ames	3		
			bar	Bacillus anthracis Ames 0581	3		
			baa	Bacillus anthracis A2012	3		
			bat	Bacillus anthracis Sterne	3		
			bah	Bacillus anthracis CDC 684	3	3	3
			bai	Bacillus anthracis A0248	3	3	3
			bce	Bacillus cereus ATCC 14579	3	3	3
			bca	Bacillus cereus ATCC 10987	3	3	3
			bcz	Bacillus cereus ZK	3	3	3
			bcr	Bacillus cereus AH187	3	3	3
			bcb	Bacillus cereus B4264	3	3	3
			bcu	Bacillus cereus AH820	3	3	3
			bcg	Bacillus cereus G9842	3	3	3
			bcq	Bacillus cereus Q1	3	3	3
			bcx	Bacillus cereus 03BB102	3	3	3
			bcy	Bacillus cytotoxis NVH 391-98			
			btk	Bacillus thuringiensis 97-27	3		
			btl	Bacillus thuringiensis Al Hakam	3	3	3
			bwe	Bacillus weihenstephanensis	3	3	3
			bli	Bacillus licheniformis ATCC 14580	1	1	1
			bld	Bacillus licheniformis DSM13	1		
			bcl	Bacillus clausii	1	1	
			bay	Bacillus amyloliquefaciens	3		
			bpu	Bacillus pumilus			
			bpf	Bacillus pseudofirmus	5		
			bmq	Bacillus megaterium QM B1551			
		Oceanobacillus	oih	Oceanobacillus iheyensis			
		Geobacillus	gka	Geobacillus kaustophilus			
			gtn	Geobacillus thermodenitrificans			
			gwc	Geobacillus sp. WCH70			
			gym	Geobacillus sp. Y412MC10	2	1	1
			gyc	Geobacillus sp. Y412MC61	2		
		Anoxybacillus	afl	Anoxybacillus flavithermus			
		Staphylococcus	sau	Staphylococcus aureus N315 (MRSA/VSSA)			
			sav	Staphylococcus aureus Mu50 (MRSA/VISA)			
			saw	Staphylococcus aureus Mu3 (MRSA/hetero-VISA)			
			sah	Staphylococcus aureus JH1 (MRSA/VSSA)			
			saj	Staphylococcus aureus JH9 (MRSA/VRSA)			
			sam	Staphylococcus aureus MW2 (CA-MRSA)	1		
			sas	Staphylococcus aureus MSSA476 (MSSA)			
			sar	Staphylococcus aureus MRSA252 (MRSA)			
			sac	Staphylococcus aureus COL (MRSA)			
			sax	Staphylococcus aureus USA300_TCH1516 (CA-MSSA)			
			saa	Staphylococcus aureus USA300_FPR3757 (CA-MRSA)			
			sao	Staphylococcus aureus NCTC8325			
			sae	Staphylococcus aureus Newman			
			sad	Staphylococcus aureus ED98			
			sab	Staphylococcus aureus RF122			
			sep	Staphylococcus epidermidis ATCC 12228			
			ser	Staphylococcus epidermidis RP62A			
			sha	Staphylococcus haemolyticus			
			ssp	Staphylococcus saprophyticus			
			sca	Staphylococcus carnosus			
			slg	Staphylococcus lugdunensis			
		Listeria	lmo	Listeria monocytogenes EGD-e			
			lmf	Listeria monocytogenes F2365			
			lmh	Listeria monocytogenes HCC23			
			lmc	Listeria monocytogenes Clip81459			
			lmn	Listeria monocytogenes 08-5578			
			lmy	Listeria monocytogenes 08-5923			
			lin	Listeria innocua			
			lwe	Listeria welshimeri SLCC5334			
			lsg	Listeria seeligeri			
		Lysinibacillus	lsp	Lysinibacillus sphaericus	1	1	1
		Exiguobacterium	esi	Exiguobacterium sibiricum			
			eat	Exiguobacterium sp. AT1b			
		Macrococcus	mcl	Macrococcus caseolyticus			
		Brevibacillus	bbe	Brevibacillus brevis	4		
		Paenibacillus	pjd	Paenibacillus sp. JDR-2			
		Alicyclobacillus	aac	Alicyclobacillus acidocaldarius			
		Lactococcus	lla	Lactococcus lactis subsp. lactis IL1403			
			llk	Lactococcus lactis subsp. lactis KF147			
			llc	Lactococcus lactis subsp. cremoris SK11			
			llm	Lactococcus lactis subsp. cremoris MG1363			
		Streptococcus	spy	Streptococcus pyogenes SF370 (serotype M1)			
			spz	Streptococcus pyogenes MGAS5005 (serotype M1)			
			spm	Streptococcus pyogenes MGAS8232 (serotype M18)	1		

			spg	Streptococcus pyogenes MGAS315 (serotype M3)			
			sps	Streptococcus pyogenes SSI-1 (serotype M3)			
			sph	Streptococcus pyogenes MGAS10270 (serotype M2)			
			spi	Streptococcus pyogenes MGAS10750 (serotype M4)			
			spj	Streptococcus pyogenes MGAS2096 (serotype M12)	1		
			spk	Streptococcus pyogenes MGAS9429 (serotype M12)	1		
			spf	Streptococcus pyogenes Manfredo (serotype M5)			
			spa	Streptococcus pyogenes MGAS10394 (serotype M6)			
			spb	Streptococcus pyogenes MGAS6180 (serotype M28)			
			soz	Streptococcus pyogenes NZ131 (serotype M49)	1		
			spn	Streptococcus pneumoniae TIGR4 (virulent serotype 4)			
			spd	Streptococcus pneumoniae D39 (virulent serotype 2)			
			spr	Streptococcus pneumoniae R6 (avirulent)			
			spw	Streptococcus pneumoniae CGSP14 (serotype 14)			
			spx	Streptococcus pneumoniae G54 (serotype 19F)			
			sne	Streptococcus pneumoniae ATCC 700669 (serotype 23F ST81 lineage)			
			spv	Streptococcus pneumoniae Hungary19A 6			
			snm	Streptococcus pneumoniae 70585			
			sjj	Streptococcus pneumoniae JJA			
			spp	Streptococcus pneumoniae P1031			
			snt	Streptococcus pneumoniae Taiwan19F-14			
			sag	Streptococcus agalactiae 2603 (serotype V)			
			san	Streptococcus agalactiae NEM316 (serotype III)			
			sak	Streptococcus agalactiae A909 (serotype Ia)			
			smu	Streptococcus mutans UA159			
			smc	Streptococcus mutans NN2025			
			stc	Streptococcus thermophilus CNRZ1066			
			stl	Streptococcus thermophilus LMG18311			
			ste	Streptococcus thermophilus LMD-9			
			ssa	Streptococcus sanguinis			
			ssu	Streptococcus suis 05ZYH33			
			ssv	Streptococcus suis 98HAH33			
			ssb	Streptococcus suis BM407			
			ssi	Streptococcus suis P1/7			
			sss	Streptococcus suis SC84			
			sgo	Streptococcus gordonii			
			seq	Streptococcus equi subsp. zooepidemicus H70			
			sez	Streptococcus equi subsp. zooepidemicus MGCS10565			
			seu	Streptococcus equi subsp. equi 4047			
			sub	Streptococcus uberis			
			sds	Streptococcus dysgalactiae			
			sga	Streptococcus gallolyticus			
			smb	Streptococcus mitis B6			
		Lactobacillus	lpl	Lactobacillus plantarum WCFS1			
			lpj	Lactobacillus plantarum JDM1			
			ljo	Lactobacillus johnsonii NCC 533			
			ljf	Lactobacillus johnsonii FI9785			
			lac	Lactobacillus acidophilus	1		
			lsa	Lactobacillus sakei			
			lsl	Lactobacillus salivarius	2	1	1
			ldb	Lactobacillus delbrueckii ATCC 11842	1		
			lbu	Lactobacillus delbrueckii ATCC BAA-365	1		
			lbr	Lactobacillus brevis	1		
			lca	Lactobacillus casei ATCC 334	1		
			lcb	Lactobacillus casei BL23	1		
			lga	Lactobacillus gasseri			
			lre	Lactobacillus reuteri DSM 20016			
			lrf	Lactobacillus reuteri JCM 1112			
			lhe	Lactobacillus helveticus			
			lfe	Lactobacillus fermentum			
			lrh	Lactobacillus rhamnosus			
			lrl	Lactobacillus rhamnosus Lc 705			
		Pediococcus	ppe	Pediococcus pentosaceus			
		Enterococcus	efa	Enterococcus faecalis	2	1	1
		Oenococcus	ooe	Oenococcus oeni			
		Leuconostoc	lme	Leuconostoc mesenteroides			
			lci	Leuconostoc citreum			
		Clostridium	cac	Clostridium acetobutylicum			
			cpe	Clostridium perfringens 13	3		
			cpf	Clostridium perfringens ATCC 13124	3		
			cpr	Clostridium perfringens SM101	3		
			ctc	Clostridium tetani E88			
			cno	Clostridium novyi			
			cth	Clostridium thermocellum			
			cdf	Clostridium difficile 630	1	1	1
			cdc	Clostridium difficile CD196	1		
			cdl	Clostridium difficile R20291	1		
			cbo	Clostridium botulinum A ATCC 3502			
			cba	Clostridium botulinum A ATCC 19397			
			cbh	Clostridium botulinum A Hall			
			cby	Clostridium botulinum A2			
			cbl	Clostridium botulinum A3 Loch Maree			
			cbk	Clostridium botulinum B Eklund 17B			
			cbb	Clostridium botulinum B1 Okra			
			cbi	Clostridium botulinum Ba4			
			cbt	Clostridium botulinum E3			
			cbf	Clostridium botulinum F Langeland			
			cbe	Clostridium beijerinckii	2	1	1
			ckl	Clostridium kluyveri DSM 555			
			ckr	Clostridium kluyveri NBRC 12016			
			cpy	Clostridium phytofermentans			
			cce	Clostridium cellulolyticum	1	1	1
		Alkaliphilus	amt	Alkaliphilus metalliredigens	1		

			aoe	Alkaliphilus oremlandii	1		
		Symbiobacterium	sth	Symbiobacterium thermophilum			
		Syntrophomonas	swo	Syntrophomonas wolfei			
		Veillonella	vpr	Veillonella parvula			
		Acidaminococcus	afn	Acidaminococcus fermentans			
		Anaerocellum	ate	Anaerocellum thermophilum			
		Desulfitobacterium	dsy	Desulfitobacterium hafniense Y51			
			dhd	Desulfitobacterium hafniense DCB-2			
		Desulfotomaculum	drm	Desulfotomaculum reducens	1	1	1
			dae	Desulfotomaculum acetoxidans			
		Pelotomaculum	pth	Pelotomaculum thermopropionicum			
		Desulforudis	dau	Candidatus Desulforudis audaxviator			
		Heliobacterium	hmo	Heliobacterium modesticaldum			
		Finegoldia	fma	Finegoldia magna			
		Anaerococcus	apr	Anaerococcus prevotii	1		
		Eubacterium	eel	Eubacterium eligens			
			ere	Eubacterium rectale			
		Unclassified Clostridi	clo	Clostridiales genomosp. BVAB3			
		Thermoanaerobacter	tte	Thermoanaerobacter tengcongensis	2		
			tex	Thermoanaerobacter sp. X514	1		
			tpd	Thermoanaerobacter pseudethanolicus	2		
			tit	Thermoanaerobacter italicus			
		Carboxydothermus	chy	Carboxydothermus hydrogenoformans	1	1	1
		Moorella	mta	Moorella thermoacetica			
		Ammonifex	adg	Ammonifex degensii			
		Caldicellulosiruptor	csc	Caldicellulosiruptor saccharolyticus	2		
		Coprothermobacter	cpo	Coprothermobacter proteolyticus			
		Natranaerobius	nth	Natranaerobius thermophilus			
		Halothermothrix	hor	Halothermothrix orenii	1	1	1
	Tenericute	Mycoplasma	mge	Mycoplasma genitalium			
			mpn	Mycoplasma pneumoniae			
			mpu	Mycoplasma pulmonis			
			mpe	Mycoplasma penetrans			
			mga	Mycoplasma gallisepticum			
			mmy	Mycoplasma mycoides			
			mmo	Mycoplasma mobile			
			mhy	Mycoplasma hyopneumoniae 232			
			mhj	Mycoplasma hyopneumoniae J			
			mhp	Mycoplasma hyopneumoniae 7448			
			msy	Mycoplasma synoviae			
			mcp	Mycoplasma capricolum			
			maa	Mycoplasma agalactiae PG2			
			mal	Mycoplasma agalactiae 5632			
			mat	Mycoplasma arthritidis			
			mco	Mycoplasma conjunctivae			
			mho	Mycoplasma hominis			
			mcd	Mycoplasma crocodyli			
		Ureaplasma	uur	Ureaplasma parvum serovar 3 ATCC 700970			
			upa	Ureaplasma parvum serovar 3 ATCC 27815			
			uue	Ureaplasma urealyticum serovar 10 ATCC 33699			
		Phytoplasma	poy	Phytoplasma OY			
			ayw	Phytoplasma AYWB			
			pml	Candidatus Phytoplasma mali			
			pal	Candidatus Phytoplasma australiense			
		Acholeplasma	acl	Acholeplasma laidlawii	1		
		Mesoplasma	mfl	Mesoplasma florum			
	Actinobac	Mycobacterium	mtu	Mycobacterium tuberculosis H37Rv			
			mtc	Mycobacterium tuberculosis CDC1551			
			mra	Mycobacterium tuberculosis H37Ra			
			mtf	Mycobacterium tuberculosis F11			
			mtb	Mycobacterium tuberculosis KZN 1435			
			mbo	Mycobacterium bovis AF2122/97			
			mbb	Mycobacterium bovis BCG Pasteur 1173P2			
			mbt	Mycobacterium bovis BCG Tokyo 172			
			mle	Mycobacterium leprae TN			
			mlb	Mycobacterium leprae Br4923			
			mpa	Mycobacterium avium paratuberculosis			
			mav	Mycobacterium avium 104	1		
			msm	Mycobacterium smegmatis	1		
			mul	Mycobacterium ulcerans	2		
			mva	Mycobacterium vanbaalenii	3		
			mgi	Mycobacterium gilvum			
			mab	Mycobacterium abscessus ATCC 19977	3		
			mmc	Mycobacterium sp. MCS	2		
			mkm	Mycobacterium sp. KMS	3		
			mjl	Mycobacterium sp. JLS	2		
			mmi	Mycobacterium marinum M	2		
		Corynebacterium	cgl	Corynebacterium glutamicum ATCC 13032 (Kyowa Ha	1		
			cgb	Corynebacterium glutamicum ATCC 13032 (Bielefeld)	1		
			cgt	Corynebacterium glutamicum R	1		
			cef	Corynebacterium efficiens	1		
			cdi	Corynebacterium diphtheriae			
			cjk	Corynebacterium jeikeium	1		
			cur	Corynebacterium urealyticum			
			car	Corynebacterium aurimucosum			
			ckp	Corynebacterium kroppenstedtii			
		Nocardia	nfa	Nocardia farcinica			
		Rhodococcus	rha	Rhodococcus sp. RHA1			
			rer	Rhodococcus erythropolis	1		
			rop	Rhodococcus opacus	1		
		Gordonia	gbr	Gordonia bronchialis			
		Streptomyces	sco	Streptomyces coelicolor	3		
			sma	Streptomyces avermitilis	1		

			sgr	Streptomyces griseus	1	1
			scb	Streptomyces scabiei		
		Tropheryma	twh	Tropheryma whipplei Twist		
			tws	Tropheryma whipplei TW08/27		
		Leifsonia	lxx	Leifsonia xyli xyli CTCB07		
		Clavibacter	cmi	Clavibacter michiganensis subsp. michiganensis		
			cms	Clavibacter michiganensis subsp. sepedonicus		
		Arthrobacter	art	Arthrobacter sp. FB24	2	
			aau	Arthrobacter aurescens	3	
			ach	Arthrobacter chlorophenolicus	1	
		Renibacterium	rsa	Renibacterium salmoninarum	2	
		Kocuria	krh	Kocuria rhizophila	1	
		Micrococcus	mlu	Micrococcus luteus		
		Rothia	rmu	Rothia mucilaginosa		
		Beutenbergia	bcv	Beutenbergia cavernae	1	
		Brachybacterium	bfa	Brachybacterium faecium	1	
		Jonesia	jde	Jonesia denitrificans	2	
		Kytococcus	kse	Kytococcus sedentarius		
		Xylanimonas	xce	Xylanimonas cellulosilytica		
		Sanguibacter	ske	Sanguibacter keddieii		
		Propionibacterium	pac	Propionibacterium acnes KPA171202		
			pak	Propionibacterium acnes SK137		
		Nocardioides	nca	Nocardioides sp. JS614	1	
		Kribbella	kfl	Kribbella flavida	7	
		Thermobifida	tfu	Thermobifida fusca		
		Thermomonospora	tcu	Thermomonospora curvata		
		Streptosporangium	sro	Streptosporangium roseum	9	
		Frankia	fra	Frankia sp. Ccl3	2	
			fre	Frankia sp. EAN1pec	1	
			fal	Frankia alni		
		Acidothermus	ace	Acidothermus cellulolyticus		
		Nakamurella	nml	Nakamurella multipartita		
		Geodermatophilus	gob	Geodermatophilus obscurus		
		Kineococcus	kra	Kineococcus radiotolerans		
		Saccharopolyspora	sen	Saccharopolyspora erythraea	2	
		Saccharomonospora	svi	Saccharomonospora viridis	1	
		Actinosynnema	ami	Actinosynnema mirum	1	
		Salinispora	stp	Salinispora tropica	5	
			saq	Salinispora arenicola	6	
		Catenulispora	cai	Catenulispora acidiphila	2	
		Stackebrandtia	sna	Stackebrandtia nassauensis	3	
		Bifidobacterium	blo	Bifidobacterium longum NCC2705		
			blj	Bifidobacterium longum DJO10A		
			bln	Bifidobacterium longum subsp. infantis ATCC 15697		
			bad	Bifidobacterium adolescentis		
			bla	Bifidobacterium animalis subsp. lactis AD011		
			blc	Bifidobacterium animalis subsp. lactis Bl-04		
			blt	Bifidobacterium animalis subsp. lactis DSM 10140		
			bde	Bifidobacterium dentium		
		Gardnerella	gva	Gardnerella vaginalis		
		Rubrobacter	rxy	Rubrobacter xylanophilus	1	
		Conexibacter	cwo	Conexibacter woesei		
		Acidimicrobium	afo	Acidimicrobium ferrooxidans DSM 10331		
		Cryptobacterium	ccu	Cryptobacterium curtum		
		Slackia	shi	Slackia heliotrinireducens		
		Atopobium	apv	Atopobium parvulum		
		Eggerthella	ele	Eggerthella lenta	1	
	Chlamydia	Chlamydia	ctr	Chlamydia trachomatis D/UW-3/CX (serovar D)		
			cta	Chlamydia trachomatis A/HAR-13 (serovar A)		
			ctb	Chlamydia trachomatis 434/Bu		
			ctl	Chlamydia trachomatis L2b/UCH-1/proctitis		
			ctj	Chlamydia trachomatis B/Jali20/OT		
			cmu	Chlamydia muridarum		1
		Chlamydophila	cpn	Chlamydophila pneumoniae CWL029		
			cpa	Chlamydophila pneumoniae AR39		
			cpj	Chlamydophila pneumoniae J138		
			cpt	Chlamydophila pneumoniae TW183		
			cca	Chlamydophila caviae		
			cab	Chlamydophila abortus		
			cfe	Chlamydophila felis		
		Protochlamydia	pcu	Candidatus Protochlamydia amoebophila		1
	Spirochaet	Borrelia	bbu	Borrelia burgdorferi B31		
			bbz	Borrelia burgdorferi ZS7		
			bga	Borrelia garinii		
			baf	Borrelia afzelii		
			btu	Borrelia turicatae		
			bhr	Borrelia hermsii		
			bdu	Borrelia duttonii		
			bre	Borrelia recurrentis		
		Treponema	tpa	Treponema pallidum subsp. pallidum Nichols		
			tpp	Treponema pallidum subsp. pallidum SS14		
			tde	Treponema denticola		
		Leptospira	lil	Leptospira interrogans serovar lai		
			lic	Leptospira interrogans serovar Copenhageni		
			lbj	Leptospira borgpetersenii JB197		
			lbl	Leptospira borgpetersenii L550		
			lbi	Leptospira biflexa serovar Patoc Patoc 1 (Paris)		
			lbf	Leptospira biflexa serovar Patoc Patoc 1 (Ames)		
		Brachyspira	bhy	Brachyspira hyodysenteriae		
	Acidobacte	Koribacter	aba	Acidobacteria bacterium	1	
		Acidobacterium	aca	Acidobacterium capsulatum		
		Solibacter	sus	Solibacter usitatus	1	
	Bacteroide	Bacteroides	bth	Bacteroides thetaiotaomicron	2	

			bfr	Bacteroides fragilis YCH46	1			
			bfs	Bacteroides fragilis NCTC9343	1			
			bvu	Bacteroides vulgatus		1		
		Porphyromonas	pgi	Porphyromonas gingivalis W83				
			pgn	Porphyromonas gingivalis ATCC 33277				
		Parabacteroides	pdi	Parabacteroides distasonis	1			
		Azobacteroides	aps	Candidatus Azobacteroides pseudotrichonymphae				
		Prevotella	pru	Prevotella ruminicola				
		Salinibacter	sru	Salinibacter ruber	1			
			srm	Salinibacter ruber	1			
		Rhodothermus	rmr	Rhodothermus marinus				
		Cytophaga	chu	Cytophaga hutchinsonii	1			
		Dyadobacter	dfe	Dyadobacter fermentans	1			
		Spirosoma	sli	Spirosoma linguale				
		Chitinophaga	cpi	Chitinophaga pinensis				
		Pedobacter	phe	Pedobacter heparinus	1			
		Gramella	gfo	Gramella forsetii				
		Flavobacterium	fjo	Flavobacterium johnsoniae	1			
			fps	Flavobacterium psychrophilum				
			fba	Flavobacteriaceae bacterium				
		Capnocytophaga	coc	Capnocytophaga ochracea	1			
		Robiginitalea	rbi	Robiginitalea biformata				
		Zunongwangia	zpr	Zunongwangia profunda				
		Sulcia	smg	Candidatus Sulcia muelleri GWSS				
			sms	Candidatus Sulcia muelleri SMDSEM				
			smh	Candidatus Sulcia muelleri DMIN				
		Blattabacterium	bbl	Blattabacterium sp. (Blattella germanica)				
			bpi	Blattabacterium sp. (Periplaneta americana)				
		Amoebophilus	aas	Candidatus Amoebophilus asiaticus				
	Fibrobacte	Fibrobacter	fsu	Fibrobacter succinogenes				
	Fusobacte	Fusobacterium	fnu	Fusobacterium nucleatum				
		Leptotrichia	lba	Leptotrichia buccalis				
		Sebaldella	str	Sebaldella termitidis	1	1	1	
		Streptobacillus	smf	Streptobacillus moniliformis	1			
	Verrucomi	Opitutus	ote	Opitutus terrae				
		Coraliomargarita	caa	Coraliomargarita akajimensis				
		Methylacidiphilum	min	Methylacidiphilum infernorum				
		Akkermansia	amu	Akkermansia muciniphila				
	Gemmatim	Gemmatimonas	gau	Gemmatimonas aurantiaca	1			
	Planctomy	Rhodopirellula	rba	Rhodopirellula baltica	1			
		Pirellula	psl	Pirellula staleyi				
	Elusimicro	Elusimicrobium	emi	Elusimicrobium minutum				
		Termite group 1	rsd	Uncultured Termite group 1 bacterium phylotype Rs-D17				
	Synergiste	Thermanaerovibrio	tai	Thermanaerovibrio acidaminovorans				
		Aminobacterium	aco	Aminobacterium colombiense				
	Cyanobact	Synechocystis	syn	Synechocystis sp. PCC6803	1			
		Synechococcus	syw	Synechococcus sp. WH8102				
			syc	Synechococcus elongatus PCC6301				
			syf	Synechococcus elongatus PCC7942				
			syd	Synechococcus sp. CC9605				
			sye	Synechococcus sp. CC9902				
			syg	Synechococcus sp. CC9311		1		
			syr	Synechococcus sp. RCC307				
			syx	Synechococcus sp. WH7803				
			syp	Synechococcus sp. PCC7002				
			cya	Cyanobacteria Yellowstone A-Prime				
			cyb	Cyanobacteria Yellowstone B-Prime				
		Thermosynechococcu	tel	Thermosynechococcus elongatus				
		Microcystis	mar	Microcystis aeruginosa				
		Cyanothece	cyt	Cyanothece sp. ATCC 51142				
			cyp	Cyanothece sp. PCC 8801	1			
			cyc	Cyanothece sp. PCC 7424				
			cyn	Cyanothece sp. PCC 7425				
			cyh	Cyanothece sp. PCC 8802	1			
		Unclassified Chrooco	cyu	Cyanobacterium UCYN-A				
		Gloeobacter	gvi	Gloeobacter violaceus	1			
		Nostoc	ana	Anabaena sp. PCC7120				
			npu	Nostoc punctiforme	1			
			ava	Anabaena variabilis				
		Prochlorococcus	pma	Prochlorococcus marinus SS120				
			pmm	Prochlorococcus marinus MED4				
			pmt	Prochlorococcus marinus MIT 9313				
			pmn	Prochlorococcus marinus NATL2A				
			pmi	Prochlorococcus marinus MIT9312				
			pmb	Prochlorococcus marinus AS9601				
			pmc	Prochlorococcus marinus MIT 9515				
			pmf	Prochlorococcus marinus MIT 9303		1		
			pmg	Prochlorococcus marinus MIT 9301				
			pmh	Prochlorococcus marinus MIT 9215				
			pmj	Prochlorococcus marinus MIT 9211				
			pme	Prochlorococcus marinus NATL1A				
		Trichodesmium	ter	Trichodesmium erythraeum				
		Acaryochloris	amr	Acaryochloris marina				
	Green sulf	Chlorobaculum	cte	Chlorobaculum tepidum				
			cpc	Chlorobaculum parvum NCIB 8327				
		Chlorobium	cch	Chlorobium chlorochromatii				
			cph	Chlorobium phaeobacteroides DSM 266				
			cpb	Chlorobium phaeobacteroides BS1				
			cli	Chlorobium limicola	1			
			pvi	Chlorobium vibrioformis				
		Pelodictyon	plt	Pelodictyon luteolum				
			pph	Pelodictyon phaeoclathratiforme				
		Prosthecochloris	paa	Prosthecochloris aestuarii				

		Chloroherpeton	cts	Chloroherpeton thalassium			
	Green non	Dehalococcoides	det	Dehalococcoides ethenogenes	1		
			deh	Dehalococcoides sp. CBDB1			
			deb	Dehalococcoides sp. BAV1			
			dev	Dehalococcoides sp. VS			
			deg	Dehalococcoides sp. GT			
		Roseiflexus	rrs	Roseiflexus sp. RS-1	1	1	1
			rca	Roseiflexus castenholzii DSM13941	1	1	1
		Chloroflexus	cau	Chloroflexus aurantiacus	5	1	1
			cag	Chloroflexus aggregans	3	1	1
			chl	Chloroflexus sp. Y-400-fl			
		Herpetosiphon	hau	Herpetosiphon aurantiacus	1		
		Thermomicrobium	tro	Thermomicrobium roseum			
		Sphaerobacterineae	sti	Sphaerobacter thermophilus	2		
	Deinococc	Deinococcus	dra	Deinococcus radiodurans	1		
			dge	Deinococcus geothermalis	1		
			ddr	Deinococcus deserti	2		
		Thermus	tth	Thermus thermophilus HB27	1		
			ttj	Thermus thermophilus HB8	1		
		Meiothermus	mrb	Meiothermus ruber	1	1	
	Hypertherı	Aquifex	aae	Aquifex aeolicus	1		
		Hydrogenobaculum	hya	Hydrogenobaculum sp. Y04AAS1			
		Hydrogenobacter	hth	Hydrogenobacter thermophilus			
		Thermocrinis	tal	Thermocrinis albus			
		Sulfurihydrogenibium	sul	Sulfurihydrogenibium sp. YO3AOP1			
			saf	Sulfurihydrogenibium azorense			
		Persephonella	pmx	Persephonella marina			
		Thermotoga	tma	Thermotoga maritima	1		
			tpt	Thermotoga petrophila			
			tle	Thermotoga lettingae	1		
			trq	Thermotoga sp. RQ2			
			tna	Thermotoga neapolitana	1		
			tnp	Thermotoga naphthophila			
		Thermosipho	tme	Thermosipho melanesiensis			
			taf	Thermosipho africanus	1		
		Fervidobacterium	fno	Fervidobacterium nodosum	1		
		Petrotoga	pmo	Petrotoga mobilis			
		Kosmotoga	kol	Kosmotoga olearia			
		Dictyoglomus	dth	Dictyoglomus thermophilum			
			dtu	Dictyoglomus turgidum			
		Thermodesulfovibrio	tye	Thermodesulfovibrio yellowstonii			
		Thermobaculum	ttr	Thermobaculum terrenum	1		
		Deferribacter	ddf	Deferribacter desulfuricans SSM1			
		Denitrovibrio	dap	Denitrovibrio acetiphilus			
Archaea	Euryarcha	Methanocaldococcus	mja	Methanococcus jannaschii	4	1	
			mfe	Methanocaldococcus fervens			
			mvu	Methanocaldococcus vulcanius			
			mfs	Methanocaldococcus sp. FS406-22			
		Methanococcus	mmp	Methanococcus maripaludis S2	5		
			mmq	Methanococcus maripaludis C5	4	1	
			mmx	Methanococcus maripaludis C6	3	1	
			mmz	Methanococcus maripaludis C7	5		
			mae	Methanococcus aeolicus	3		
			mvn	Methanococcus vannielii	5		
		Methanosarcina	mac	Methanosarcina acetivorans	15		
			mba	Methanosarcina barkeri	7		
			mma	Methanosarcina mazei	9	1	
		Methanococcoides	mbu	Methanococcoides burtonii	6		
		Methanohalophilus	mmh	Methanohalophilus mahii			
		Methanosaeta	mtp	Methanosaeta thermophila	6		
		Methanospirillum	mhu	Methanospirillum hungatei	3		
		Methanocorpusculum	mla	Methanocorpusculum labreanum	7		
		Methanoculleus	mem	Methanoculleus marisnigri	7		
		Methanoregula	mbn	Candidatus Methanoregula boonei	5		
		Methanosphaerula	mpl	Candidatus Methanosphaerula palustris	6		
		Methanocella	mpd	Methanocella paludicola			
		Methanobacterium	mth	Methanobacterium thermoautotrophicum	3		
		Methanosphaera	mst	Methanosphaera stadtmanae	2		
		Methanobrevibacter	msi	Methanobrevibacter smithii ATCC 35061	1		
			mru	Methanobrevibacter ruminantium			
		Methanopyrus	mka	Methanopyrus kandleri	4		
		Archaeoglobus	afu	Archaeoglobus fulgidus	12	1	1
			apo	Archaeoglobus profundus			
		Ferroglobus	fpl	Ferroglobus placidus			
		Halobacterium	hal	Halobacterium sp. NRC-1			
			hsl	Halobacterium salinarum R1	15	1	1
		Haloarcula	hma	Haloarcula marismortui	16	6	5
		Haloquadratum	hwa	Haloquadratum walsbyi	14	1	1
		Natronomonas	nph	Natronomonas pharaonis	9		
		Halorubrum	hla	Halorubrum lacusprofundi	15	3	3
		Halorhabdus	hut	Halorhabdus utahensis	14	3	3
		Halomicrobium	hmu	Halomicrobium mukohataei	14	6	5
		Haloterrigena	htu	Haloterrigena turkmenica			
		Natrialba	nmg	Natrialba magadii	17	3	3
		Haloferax	hvo	Haloferax volcanii			
		Thermoplasma	tac	Thermoplasma acidophilum	7	4	4
			tvo	Thermoplasma volcanium	7	3	3
		Picrophilus	pto	Picrophilus torridus	7	4	4
		Pyrococcus	pho	Pyrococcus horikoshii	11	3	3
			pab	Pyrococcus abyssi	10	2	1
			pfu	Pyrococcus furiosus	11	3	3
		Thermococcus	tko	Thermococcus kodakaraensis	8	2	2
			ton	Thermococcus onnurineus	11	1	1

			tga	Thermococcus gammatolerans	10	3	3
			tsi	Thermococcus sibiricus			
		Aciduliprofundum	abi	Aciduliprofundum boonei	8		
		Rice Cluster I	rci	Uncultured methanogenic archaeon RC-I			
	Crenarcha	Aeropyrum	ape	Aeropyrum pernix	6		
		Staphylothermus	smr	Staphylothermus marinus	3	1	
		Ignicoccus	iho	Ignicoccus hospitalis	4		
		Desulfurococcus	dka	Desulfurococcus kamchatkensis	4		
		Hyperthermus	hbu	Hyperthermus butylicus	6		
		Sulfolobus	sso	Sulfolobus solfataricus	12		
			sto	Sulfolobus tokodaii	20		
			sai	Sulfolobus acidocaldarius	14	1	1
			sis	Sulfolobus islandicus L.S.2.15	19		
			sia	Sulfolobus islandicus M.14.25	12		
			sim	Sulfolobus islandicus M.16.27	16		
			sid	Sulfolobus islandicus M.16.4	16		
			siy	Sulfolobus islandicus Y.G.57.14	17		
			sin	Sulfolobus islandicus Y.N.15.51	15		
			sii	Sulfolobus islandicus L.D.8.5			
		Metallosphaera	mse	Metallosphaera sedula			
		Pyrobaculum	pai	Pyrobaculum aerophilum	11	1	
			pis	Pyrobaculum islandicum	5		
			pcl	Pyrobaculum calidifontis	9		
			pas	Pyrobaculum arsenaticum	11		
		Caldivirga	cma	Caldivirga maquilingensis	8	2	2
		Thermoproteus	tne	Thermoproteus neutrophilus		1	
		Thermofilum	tpe	Thermofilum pendens	11	4	4
	Thaumarcl	Nitrosopumilus	nmr	Nitrosopumilus maritimus	10	1	1
	Nanoarcha	Nanoarchaeum	neq	Nanoarchaeum equitans	2	1	1
	Korarchae	Korarchaeum	kcr	Candidatus Korarchaeum cryptofilum	6	2	1